WEST Search History

DATE: Tuesday, September 16, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USP	T,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ	1	
L30	L29 AND human-growth-hormone	0	L30
L29	L28 AND human insulin	236	L29
L28	L27 NOT chimera	1018	L28
L27	L26 AND fusion protein	2521	L27
L26	L24 NOT Rosen-Craig.IN.	2900	L26
L25	L24 NOT Rosen-Craig.IN/	2901	L25
L24	L23 NOT Ashkenazi-Avi.IN.	2901	L24
L23	L22 NOT Rosen-Craig-A.IN.	2971	L23
L22	L17 NOT Ashkenazi-Avi-J.IN.	3165	L22
L21	L20 AND human insulin	124	L21
L20	L19 AND chimeric protein	321	L20
L19	L18 AND fusion protein	1654	L19
L18	L17 AND ((530/300 530/350)!.CCLS.)	1689	L18
L17	L16 AND L10	3281	L17
L16	L15 AND human growth hormone	5184	L16
L15	insulin	45978	L15
L14	L13 AND hGH	119	L14
L13	L12 AND human insulin	664	L13
L12	L11 AND insulin	3281	L12
L11	L10 AND human growth hormone	4467	L11
L10	(chimeric OR fusion protein OR chimera)	49651	L10
L9	L8 AND hGH	143	L9
L8	L2 AND insulin	4231	L8
L7	L2 AND insulin AND human-growth-hormone	0	L7
L6	((C07K/)!.IPC.)	8	L6
L5	(C07K)	63212	L5
L4	((C07K/5)!.CCLS.)	0	L4
L3	C07K ((5/00)!.CCLS.)	0	L3
L2	((530/300 530/350)!.CCLS.)	13606	L2
L1	(530.CCLS.)	0	L1

END OF SEARCH HISTORY

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5 ; Search time 34.4229 Seconds (without alignments) 225.942 Million cell updates/sec
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22. (SIDSI) quodata ygeneseqy qeneseqp -embi, /AA1990. DAT:
23. (SIDSI) quodata ygeneseqy qeneseqp -embi, /AA290. DAT:
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25. (SIDSI) quodata ygeneseqy qeneseqp -embi, /AA290. DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           OM protein · protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			DB	20	20	20	20	3.0	20	10	20	10
		Query	Length	5.	32	107	134	0.71	150	192	192	261
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   protein, which contains a thrombin recognition site, and buman beta nerve
             growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91299).
                                                                                                                                                  Saps
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                                                                                                                                                                                                                                                                                                                                                                                                  Insulin; precursor; growth hormone; chaperone; intramolection;
folding; conformation; chimeric protein; cleavable; recombinant;
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                                                                                                                                                                                           100.0%; Score 260; DB 10; Length 140; 190.0%; Pred, No. 7.3a-25; ive 0; Mismatches 6; Indels 6
                                                                                                                                                                             1 MEPTIPLSRLFDNAMLRAHRLHQJAFDTYQEFEBAYIPKEQKYSFLQNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 30-31; 46pp; English
                                                                                                                                                                                                                                                                                AAY42861 standard; protein; 150 AA.
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                                                                                                                                 190. Similarity 100. 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant vector contq. fusion protein - consisting of human growth hormone or deriv. Ligated to foreign protein, for stability
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                                      Length 150:
                                                                                                               1 MFPTIPLSRLFUNAMLRAHRLHQLAFDTYQEFEEAYIPKFQKYSFLQNP
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                                      , DB 20;
7.9e-25;
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                                    100.0%; Score 260; 5
100.0%; Pred. No. 7.9
ive 0; Mismatches
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                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Human growth hormone.
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Matches 49; Conserv
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es 49; Conserv
150 AA;
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06-FEB-1996
61-NOV-1989
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Gaps

5 49

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variant or human prolactin
                                                       (REGC ) UNIV CALIFURNIA
                                                               WPI; 1999-045192/04.
N-PSDB; AAX01706.
                                                   13-MAY-1997;
                                      W09851323-A1
                                              12-MAY-1998;
                                                                                                                                              dysfunction
                                          8561-ACN-61
                                                           Martia: JA,
                                                                                                                                                   Sequence
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N-terminal end (1st region), a 3 amino acid sequence representing thrombin recognition site, and human beta nerve growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatric dementia and ether nervous disorders, and can be released from the fusion process by incubation with thrombin (see AAN90577-8, AAP91034,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human nerve growth factor gene encoding fusion protein having cleavage site for thrombin, useful for treating geriatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human nerve growth factor and human growth hormone fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human nerve growth factor: lusion protein; thrombin;
gerlatzic dementia: nervous disorders; human growth hormone.
                                                                                1 MEPTIFISHLFONAMERAHREHQIJAFDTYQEFFRAYIPKFOKYSFLONP
                                                                                                                       1 MEPTIPISAS FONDAMS AND THE PROPERTIES OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP
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       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 250; DB 10;
Pred. No. 1.5e-24;
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           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP61033 standard: Protein; 262 AA.
                                                                                                                                                                                                                                                                                                                                          AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
           6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (tirst entry).
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141.143
144..261
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               49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Rest Local Similarity
Warnhes 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-243092/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOYJ ) TOSOH CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 - DEC - 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohtsuka E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAP91299;
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Region
Region
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               Matches
                                                                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel human anti-anglogenic peptides derived from 10 to 150 consecutive amino acids selected from the N-terminal end of from 10 to 150 consecutive amino acids selected from the N-terminal end of from 10 to 150 consecutive amino acids selected from the N-terminal end of formone variant (hGH-V), or human probactin. Such peptides (i) inhibit capillary endothelial cell proliferation and organisation (ii) inhibit angiogenesis in chick choice lantoin membrane and (ii) binds to at angiogenesis in chick choice lantoin membrane and (iii) binds to at angiogenesis in chick choice lantoin does not bind nearth (ii) binds to at diagonating prequancy. The prolactin or hGH-V. The invention disc describes a method for diagnosing a probable abnormality of placental vascularisation of a patient or growth in a patient or formation or growth in a patient or for peptides can be used for prevention or growth in a patient or for peptides can be used for prevention arthritic such as rheumatoid arthritis, atheroscitative relinopathy such as those pocurring carthritis, atheroscitative relinopathy such as those pocurring such as importing your acidative relinopathy, macular degeneration, granulations such as those pocurring such as hypotytrophic scars or keloid scars, necowasciar glaucoma, collar the process.
                                                                                                                                  Human; anti-anglogente: prolactin; placental lactonen; hit; angloseness; growth hormone; hGB; hGB-V; capiliary endothelial cell proliteration; blacental vascularisation; prenancy; incentent, arribogene diseased; tumour; inhibitor; malignant, anglofibroma; arteriovenous malignant; anglofibroma; arteriovenous malignant; anglofibroma; arteriovenous malignant; ordinopathy; mentat dependantisation; granulation; glancoma; ochica; uveklis; iractine; osiariweher synifone; psoriasis; fibroplasia; scieroderma; Kaposi's sateoma; vascular adhesion; quene therapy; pre-eclampsia; intrastictine growth retardation; placental dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyogenic glaucoma, recrolental fibrioplasia. Sciencederra, Solid turours, Kaposi's sarcoma, trachoma, vascular adhosions, chronic variosse ulcers. leukaemia, and reproductive disorders such as follicular and luteal cysta and choriocarcinoma. They can also be used as scitracceptive agents. INA encoding the peptides can be used in gene therapy. The measurement of abnormal levels of N-terminal fragments of hGB, FGH-V, prolactic or hEC can be used in assays for impairment of vascular development associated with pre-eclampsia, intrauterine growth retardation, and placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New anti-angiogenic peptides - comprise N-terminal tragments of human placental lactogen, human growth hormone, growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 192:
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Pred. No. 1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiner Rl;
                                                                                Human anti-angiogenic peptide hGH Met-1Phe191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 49; 87pp; English.
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100.0%;
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08-JUN-1999 (first entry)
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Query Match Best Local Similarity

192 AA;

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The protein is produced by fusing DNA encoding BDF (IL-) with DNA encoding BSF-2 (IL-5) and ligating the product into an expression vector Sec also AAR05311 and AAR05313.
                                                                               can be produced as this fusion protein. It is purified by contacting a gel having a cation exchange qp. with the fusion protein, in the presence of urea. The purified protein is useful in a medicament for treating disorders of the nervous system, eg dementia. (Updated on 25-MAR-2063 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-6; B-cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prepn. of human B-cell differentiation factor - from specified DNA sequence segment, by recombinant DNA technique, gives protein of specified amino acid sequence.
     in presence
                                                                                                                                                                                     ch 100.0%; Score 260; DB 12; Length 262; 1 Similarity 100.0%; Pred. No. 1.5e-24; 49; Conservative 6; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 310;
                                                                    A recombinant human nerve growth factor beta subunit-contg.
                                                                                                                                                                                                                                                          1 MEPTIPLSRIFDNAMBRAHKLHQLAFDIYQEFBEAYIPKEQKYSFLQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFPT12LSRLFDNAMLRAHRLHQLAFDTYQEFEEAY1PKEQKYSFLQNP
                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein of B-cell stimulatory factor-2 and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
 by contacting with yel having cation exchange gp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 260; DB 11;
ilarity 100.0%; Pred. No. 1.8e-24;
Conservative 0; Mismatches 0;
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                                         Disclosure ; fig 1; 7pp; Japanese
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                                                                                                                                                                                                                                                                                                                                      AARC3255 standard; protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                       B-cell stimulatory factor-2; i
interleukin-5; fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation factor
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                                                                                                                                                                                                  Best Local Similarity
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Matches 49; Comserv
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                                                                                                                                                             262 AA:
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               urea
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AARC 4255
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human growth hormone/human narve growth factor beta fusion protein
                                                                                                                                                                                                                                                                                                                                                           The protein is a direct translation of the upstream typptophan promoter-operator lacking its attenuation sequence and human beta-NGF sequence. The product may be efficiently expressed from transformed E.coii expression system.
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1. MPPTIPLSRLEDNAMIRAHALHQLAFOTYQEFEBAYIFKFGKYSFLONP 49
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100.0%; Score 260; DH 7; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 49; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                              - used in produ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                            Gene segment of human nerve growth factor - a NGF-producing recombinant Escherichia strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hGH; hNGF; nervous system diseases; dementia
           Human beta-nerve growth factor gene product.
                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Claim 32; Page 482; 71pp: Japanese.
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(first entry)
                                       Beta-NGF; E.coli; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAN63816-7,
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                                                                                                                                                                                                                                                                   WPI; 1986-281696/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                            262 AA;
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                                                                                                                                                                                                                                       (OISU/) OTSUKA
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                                                                                                                                                                                                              09-MAR-1985;
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                                                                   Homo sapions
                                                                                                                                                                                     09-MAR-1985;
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25-JUN-1991
                                                                                                                                                           11-SEP-1986
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                                                                                                        Protein
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The polypeptide (AAFB1226) with somatomedia-like activity and the DNA (AANBF05) emcoding it are claimed. A Met residual gp. may be added to the N-terminal. The polypeptide acts on the bone structure of mammals, including humans, to promote bone growth. The polypeptide has high production rate and is easily extracted from bacterial culture medium and retined for use as a bone growth accelerator.
                                                                                                                 Recombinant human growth hormone having collagenase recognition region
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEPTIPLSKLFONAMLKAHRLHQLAFDTYQEFEEAYIPKSOKYSFLQNP
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                                                                                                                                                                                                              The invention relates to recombinant human growth hormone
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide with sematomedin-like activity - by culturing bacterium transformed by plasmid contq. segment with specified DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of protein with somatomedin-like activity.
                                                                                                                                                                                                                                                                                                                                Score 256; DB 23;
Pred. No. 3.5e-24;
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2(1): Page 609: 9pp: Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP81226 standard; protein; 138 AA.
                                                                                                                                                                  Disclosure: Fig 3: 8pp: Korean.
                                                                                                                                                                                                                                       collagenase recognition region.
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                                                                                                                                                                                                                                                                                                                                98.5%;
98.0%;
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Sest Local Similarity
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N-PSDB; AAN81605.
                                              WPI: 2002-185396/24
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                                                                                                                                                                                                                                                                                   204 AA;
    Scag YH;
                                                                       N-PSDB; ABL55999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP63167798-A
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20-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preps. of human B-cell differentiation factor - from specified that sequence segment, by recombinant DNA technique, gives protein of specified amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEPTIPLSKLEDNAMLKAHFLHQLAFDTYQEFEEAYIPKEGKYSFLGNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 144:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human growth hormone with collagenase recognition site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human: growth hormone; collagenase; recognition site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 257; DB 11;
Pred. No. 1.8e-24;
I; Mismatches 0;
                                                                                                                                                                                   Segment of Bicell stimulatory factoric (IL-5).
                                                                                                                                                                                                                                  B-cell stimulatory factor-2: interleukin-5.
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                                            AAR05313 standard; protein; 144 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 1990-062207/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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1 FPTIPLSRLFDNAMLRAHRJAQEAFDIYQEFBRAYIPKBQKYSFLQNP 48

Search completed: September 15, 2003, 12:00:56 Job time : 35.4229 secs

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OM protein - protein search, using sw model

September 15, 2005, 11:87:40; Search time 11.2401 Seconds (without alignments) [84.449 Million cell updates/sec Run on:

US-09-423-100-1 Title: Perfect score: Sequence:

Scoring table:

BLCSUM62 Gapop 10.6 , Gapext 0.5

328717 seqs, 42310858 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2003000003

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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| CGG12_6/ptodata//laa/5A_COMB.pup:*
| CGG02_6/ptodata//laa/5B_COMB.pup:*
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SHAMARIES

Length DB ID 192 US-08-093-563-1 194 US-08-284-878-5 194 US-08-284-878-5 194 US-08-383-611-4 194 US-08-384-611-4 194 US-08-384-611-4 194 US-08-384-878-5 195 US-08-459-906-4 197 US-08-459-906-4 198 US-08-459-906-4 198 US-08-458-871-1 199 US-08-284-878-1 199 US-08-284-878-1 199 US-08-184-582-7 199 US-08-184-582-8 199 US-08-184-582-8 199 US-08-184-582-8 199 US-08-184-582-8 199 US-08-184-582-8 199 US-08-184-586-24 199 US-08-184-586-24 199 US-08-184-586-24 199 US-08-184-586-24 199 US-08-184-586-24 199 US-08-184-582-8 199 US-08-185-753-26	Result		* Query			SUMMARIES	
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Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Patent No. 5210180 Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli	0.5-0.5 3310-4 0.5-0.5 388-2670-2 0.5-0.5 388-2670-2 5.215180-1 0.5-0.7 6.21-1970-2 0.5-0.8-38.3-611-1 0.5-0.9-1.0.5-65.1 0.5-0.9-1.0.5-65.1 0.5-0.9-1.0.5-65.1 0.5-0.9-1.0.5-65.1 0.5-0.9-1.0.5-65.1 0.5-0.8-0.90-774-2 0.5-0.8-0.90-774-2 0.5-0.8-0.90-774-6 0.5-0.8-0.90-774-6 0.5-0.8-0.90-774-6		11111111111111111111111111111111111111		00000000000000000000000000000000000000	こうろのひののろうの なみななななな
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5,6	US-08-363-982-2	4 -4	193	61.3	159.5	36
Patent No. 52:0180	5215180-1	w,	161	62.3	159.5	ج ر ا
Sequence 2, Applia	US-06-277-720-2	٠,	190	61.3	159.5	3.5
Sequence 4, Appli	US-07-963-331D-4		161	52.	261.5	. 7 ;
Sequence 1, Appli	US-08-990-774-1	-,7	176	63.1	154	0
Sequence 1, Appli	CS-08-791-728-1	(¥1	176	63.1	164	67
Sequence 8, Appli	US-08-468-824-8	٠.,	131	63.3	164.5	82

ALIGNMENTS

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APPLICANT: DeBoer, Horman A.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Seeburg, Peter H.
ITLE DE INVALION: DNA for Expression of Bovine Growth Hormome NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
KEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER READBLE FORM:
KEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible CPERAING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Pathn (Gonentoch) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/093,383 FILING DATE: 14-JUL: 1993 CLASSIFICATION DATA: APPLICATION NUMBER: 07/29824 FILING CATE: 05-APR-1986 FILING DATE: 05-APR-1988 FRICK APPLICATION NUMBER: 6/632361 FILING DATE: 19-JUL: 1984 BRIDGATION NUMBER: 6/632361 FILING DATE: 19-JUL: 1984 BRIDGATION NUMBER: 06/303627 FILING DATE: 18-SSP-1981 AFFORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                            ADDRESSE: Genentech, Inc.
STREET: 460 Point San Brino Blvd
CITY: South San Francisco
STATE: CAlitornia
COUNTRY: USA
                  Sequence 1, Application 05/08093383
; Patent No. 5489529
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Johnston, Sean A. REGISTRATION NUMBER: P35,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910/371-7168
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415/225-3552
TELEPAX: 415/952-9881
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05-08-093-383-1
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us-09-423-100-1.rai

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Gaps
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PPLICANT: Sedon, Andrew P.
TILLE OF INVENTION: Stabilization of Somatotropins and Other
TILLE OF INVENTION: Proteins by Modification of Cysteine Residues
TILLE OF INVENTION: Proteins by Modification of Cysteine Residues
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanomid Company
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSKLFBNAMLKAHKLHQLAFDTYQEFEEAYIPKEGKYSFLQNP
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAILA:
ARRENT APPLICATION DAILA:
ARRENT APLICATION 1014:
ARRENT APLICATION 1014:
ARRENT APLICATION 1014:
ARRENT APLICATION: 514
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                                                                                                                     NAME: Tsevdos, Escelle J.
RESIENATION NUMBER: 31,145
REPERENCE/DOCKET NUMBER: 31,278-01
TELECOMMUNICATION INFORMATION:
FELENHONE: 203-321-2971
TELEX: 203-710-474-4659
INFORMATION FOR SEQ LE NO: 4:
SEQUIENCE CHARACTERISTICS:
LENGTH: 194 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3247
                         PRICK APPLICATION DATA:
APPLICATION NOMBER: US 07/766.142
FILLNG DATE: 25-8EP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/04459906
Fatent No. 6010999
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buckwalter, Brian L.
Cady, Susan M.
Shieh, Hong-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Webster, Darryl L. REGISTRATION NUMBER: 34,276
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INFORMATION FOR SEQ ID NO: 4:
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amino acid
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NOLECULE TYPE: proLein
US-08-459-906-4
                                                                                                                                                                                                                                                                                                                                                                                                               MCLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey COUNTRY: U.S.A. ZIP: 07470-8426
                                                                                                                                                                                                                                                                                                                                                                                                   linear
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APPLICANT:
APPLICANT:
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US-08-459-906-4
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APPLICANT: Statement Martha Superrero
APPLICANT: Statement Hard Superrero
APPLICANT: Saldana, Hugo Barrera APPLICANT: Saldana, Hugo Barrera APPLICANT: Salvado, Jose Maria Viader
APPLICANT: Salvado, Jose Maria Viader
TITLE OF INVENTION: Generically Meditiod Methylotrophis P. pustures Served CORRENT FILE REFERENCE: 1829,001000 of the Human Growth Horsone
FILE REFERENCE: 1829,001000 of the Human Growth Horsone
CURRENT APPLICATION NUMBER: US/09/284,878
PRIOR FILING DATE: 1997-10-21
NUMBER OF SED 16 NOS: 9
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Daley, Michael J.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Scheh, Hong-Ming
APPLICANT: Scheh, Poter
APPLICANT: Scheh, Poter
TITLE OF INVENTION: Stabilization Of Somatotropins And Other
TITLE OF INVENTION: Proteins By Modification 31 Cysteine Residues
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                                                                                                                                                                      1 MEPTIPLSRUFDNAMURABRUHGLAFDTYQEFBBAYIPKEÖKYSFLONP 49
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                                                                     Query Match
100.0%; Score 260; EH 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.66-30;
Matches 49; Conservative 6; Mismatches 6; Indels 6
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.1%: Score 255: DB 4: E. Best Local Similarity 106.0%: Pred. No. 2.4e-29; Matches 48; Conservative 0; Mismatches 0;
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1937 West Main Street, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US/08/383,621
06-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-383-621-4
; Sequence 4, Application US/08333621
; Patent No. 5951972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Connecticut
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-09-284-878-5
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 191
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US-09-284-878-5
                    US-C8-093-383-1
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APPLICANT: Newgard, Christopher B.
APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: Clark, Samuel A.
APPLICANT: Thispen, Anice E.
APPLICANT: Thispen, Anice E.
APPLICANT: Kruse, Fred
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROIEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE ADDRESS:
                                              APPLICANT: Quaade, Christian
APPLICANT: Kruse, Fred
APPLICANT: MCGATTY, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE ADDRESS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSRLPDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version: #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/784,582
FLING DATE: Concurrently Herewith
CLASSIFICATION: 435
PATOR APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PRIOR RPPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PAPLICATION NUMBER: US 60/028,427
APPLICATION NUMBER: US 60/028,427
ALING DATE: 15-0AN-1996
ATORNEY/AGENT INFORMATION:
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100.0%; Pred. No. 2.9e-29;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Highlander, Steven L. RESISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: UTSD:514 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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Patent No. 6194176
Clark, Samuel A.
Thigper, Anice E.
Quadde, Christian
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TELEFAX: 512/44-7577
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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amino acid
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Host Local Similarity 105.(
Matches 48: Conservative
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                                                                                                                                                                                                                                                                                Texas
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                                                                                                                                                                                                                                                                                              COUNTRY: US
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US-68-785-271-10
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       APPLICANT:
APPLICANI:
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CIIY: H
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APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Quaado, Christian
APPLICANT: Kruse, Fred
TITLE OF INVENTION: Recombinant Expression of Proteins From TITLE OF INVENTION: Secretory Cell Lines
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnoid, White & Durkoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPTIPLSRLEDNAMLRAHRLHQLAFDTYQRFEEAYIPKEQKYSFLQNP 49
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                                                                                                                                          4 FPTIPLSRLEDNAMSRAERLEQLAEDTYGEFEEAYIPKEGKYSFLQNP 51
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                            Length 1947
                                                                        C; Indels
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CDERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/03/589.028
FYLING DATE: CONCUTTENT, HETEWITE
                         98.1%: Score 255: FH ↔ : 100.0%; Fred. No. 2.56 ∠9;
Live C: Mismatches C:
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ATORNEY/AGENT INFORMATION:
NAME: #19thlander, Stewon L.
REGISTRATION NUMBER: 47.542
REFERENCE/DOCKET NUMBER: GISD:426/HYL
ITELECOMMUNICATION INFORMATION:
ITELEPRAX: (512) 474-7577
ITELERAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-784-582-10
Sequence 10, Application US/06:84582
Patent No. 6110707
GENERAL INFORMATION:
APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Philippe A.
APPLICANT: No. 6110707mlugton, Karl D.
                                                                                                                                                                                                                                                                                                                                        Newgard, Christopher B.
Halban, Philippe
No. 6087129mington, Karl D.
Clark, Samuel A.
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                                                                                                                                                                                                                                                                  Sequence 10, Application US/08589028
Patent No. 6087129
GENERAL INFORMATION:
APPLICANT: Halban, Christopher E
APPLICANT: Halban, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 217 amino acids TYPE: amino acid
                                                 Best Local Similarity 100.
Matches 48; Conservative
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Matches 48; Conserv
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ZIP: 77210-4433
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STREEF: F. .
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APPLICANT: Saldana, Martha Guerrero
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
APLICANT: Saldana, Hugo Barrera
APLICANT: Saldana, Hugo Barrera
APLICANT: Saldana, Hugo Barrera
APLICANT: Saldano, Jose Maria Viader
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for t.
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for t.
TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone
FILE REFERENCE: 1829.0010000
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/MX97/00033
PRIOR APPLICATION DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FPTIPLSKLFUNAMLRAHRIHQLAFUTYQEFEEAYIPKEQKYSFLUNP 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.1%; Score 255; Db 3; Length 217;
100.0%; Pred. No. 2.9e-29;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
.COCATION: 192..210
.THEN INFORMATION: /cote* "The peptides above are
.THEN THFORMATION: depicted in Figure 1"
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Patent No. 6391585
GENERAL INFORMATION:
APPLICANT: HANLL SYNTHETIC FIBER CO., LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
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  TELECOMMUNICATION INFORMATION:
TELEFAX: 415-496-1200
                                         TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRACIER STICS:
LENGTH: 217 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.1
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Rest Local Similarity 150.00
Rest Local 48; Conservative
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Pest Local Similarity 100.0
Matches 48: Conservative
                                                                                                                                                        single
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133..153
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TYPE: PRT
CRGANISM: Homo saplems
                                                                                                                                                                                                                                            NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                      94..115
                                                                                                                                                                               inear
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COCATION:
PEATURE:
                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                      :NCITADO:
                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-39-284-878-1
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                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Pernando
APPLICANT: Razan, J. Fernando
APPLICANT: Kastclein. Robert A.
TITLE OF INVENTION: MUTATIONAL, VARIANTS OF MAMM.IAN PROTEINS
NUMBER OF SEQUENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPTIPLSRLFUNAMLRAHRLHQLAFOTYQEFEBAYIPKEQKYSFLONP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Longth 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                            MEDIJM TYPE: Floppy disk
COMPUTER: 18M PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATOMIN PC-DOS/MS-DOS
SOFTWARE: PATOMIN PC-DOS/MS-DOS
SOFTWARE: PATOMIN BC:CASE #1.0, Version #1.45
APPLICATION NUMBER: US/08/785,271
FILING DATE: Concurrently Herewith:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/589,028
FILING DATE: US-JAN-1996
ATTOMY AGENT INFORMATION:
ANAMORE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.80 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/CB/759,628 FILING DATE: US-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 255; DB 3; I
Pred. No. 2.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0% Pred. No. 2.99
Onservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 NAME: Highlander, Steven L.
REGISSRATION NUMBER: 37,642
REPERENCE/DOCKET NUMBER: (TSD:513
TELECOMMUNICATION TREOEMATION:
TELECHONE: 512/418-3000
TELECHONE: 512/418-3000
INFORMATION: FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 66/608,574
FILING DATE: 06-DEC-1995
ATTORNEY/ASENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,(90
REFERENCE/DOCKET NUMBER: DX05520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/U8759628
Patent No. 6225446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 217 amino acids
                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
SIATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
STATE: Texas
                                         77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-785-271-10
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US-08-759-628-11
                    COUNTRY:
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                                                APPLICANT: Clark, Samuel A.
APPLICANT: Thigper, Anice E.
APPLICANT: Thigper, Anice E.
APPLICANT: Mcdae, Christian
APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE ADDRESS:
                          2 PPTIPLSRLFDNAMLRAHRIHGLAFDTYGEFEEAYIPKEGKYSFLONP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FPIIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%; Score 255; DB 3; Length 274; 106.0%; Pred. No. 3.8e-29; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC COMPATIDLE
COMPUTER: IHM PC COMPATIDLE
COMPUTER: IHM PC COMPATIDLE
COMPUTER: IHM PC COMPATIDLE
COMPUTER: PATENTIAN PC DOS/MS-DOS
SOFTGARE: PATENTIAN PC DOS/MS-DOS
SOFTGARE: PATENTIAN DATA:
APPLICATION NUMBER: US/08/427
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-14AN 1996
ATTCHNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              Halban, Philippe A.
No. 6110707mington, Karl D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Highlander, Steven L. BEGISTRATION NUMBER: 37.642 BEFENDE/LOCKET NUMBER: JTSD:514 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          Newgard, Christopher B.
                                                                                                                                                           fg-08-784-582-71
; Sequence 71, Application US/08784582
; Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-784-592-73

/ Sequence 73, Application US/08784582
Pattent No. 6110707

: GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Rest Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : TOPOLOGY: linear
US-08-784-582-71
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDONESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77210
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                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                              efficient expression vector from Sacharomynes corPVisiae
                                                                                                               SEONG, Baik-Lin INVENTION: Process for proparting recombinant proteins using Lightly
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APPLICANT: Kodo, Masaaki
TITLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
TITLE OF INVENTION: PREPARING USEFUL POLYPEPTICES THROUGH EXPRESSION OF THE
TITLE OF INVENTION: DNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 98.1%; Score 255; DB 4: Length 241; Best Local Similarity 100.0%, Pred. No. 3.38-29; Matches 48; Conservative 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.18; Snore 255; DB 4; Length 245; 100.0%; Pred. No. 3.38-29; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                               NUMBER OF SEQUENCES: 26
CORRESPONDENCE AUDRESS:
ADDRESSE: BACHMAN & LAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street
CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/424,620B
ELING DATE: 24-NO, 6391585-1999
INFORMATION FOR SEQ 1D NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 382,1028
CURRENT APPLICATION NUMBER: 034/69/280,030A
CURRENT FILING LATE: 1999-03-26
EARLIER APPLICATION NUMBER: JF:0-67339/1938
EARLIER FILING DATE: 1998-03-11
SUMBER OF SEQ ID NOS: 66
SOFTWARE: PATCHIIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IRM
CPERATING SYSTEM: WINDOWS 95/98
SOFTWARE: MS WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: PROTEIN

SEQUENCE DESCR:PTION: SEQ ID NO: 25:
US-09-424-6208-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66. Application US/09280030A
Patent No. 6506595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 241 amino acids
TYPE: amino acid
                   MCON, Jac-Woong
BAE, Cheon-Soon
                                                               YANG, DOC-SUK
LEE, Jee-Won
SEONG, Baik-Lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sato, Seiji
APPLICANT: Higashikuni, Naohiko
JANG, Ki Ryong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                    STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 06510-2802
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                                                                                                                                        TITLE OF
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US-09-280-030-66
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LENGTH: 245
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O
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                                                                                                                                                                                                                                                                                                           | FPITPLSREFUNASLRAHRLEGLAFDIYQEFEEAYIPKEQKYSFLQNP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FPTIPESREEDNAMIRAHREHQLAFOTYQEFEEAYIPKFOKYSFLONP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 249; DB 4; Length 191; 97.9%; Pred. No. 1.8e-28; rative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quory Match 95.8%, Score 249, DB 1; Length 217; Best Local Similarity 97.9%, Pred. No. 2.18-28; Matches 47; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSEN: E1 AL.
TITLE OF INVENTION: Human Growth Hormone
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: GARRILA, BARNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
CCUMPRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September 15, 2003, 12:05:30 cbb time : 12.2401 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,756C
FILING DATE: January 27, 1994
CLASSIEICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325800-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETIE COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08187756C
Patent No. 5597709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
:NFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACIERISTICS:
LENGTH: 217 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 217 AMINO ACIDS
AMINO ACID
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                                                                                                                                 Udery Match
Bost Local Similarity 97,99
Matchas 47, Conservative
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                                                               ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08 187-756C-4
   LENGTH: 191
                                                                                           US:09-465-461-1
                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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( Y
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US-09-465-461-1

US-09-465-461-1

Sequence 1, Application US/09465461

Parent No. 6346444

GENERAL INFORMATION:

APPLICANT: CHAPPEL, SCOTT

TILLE OF INVENTION: after hematopoletic stem cell transplantation in building price in building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ڌ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                           APPLICANT: Thispen, Anice E. APPLICANT: Thispen, Anice E. APPLICANT: Quaade, Christian APPLICANT: Quaade, Christian APPLICANT: Kruse, Fred TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FEDM TITLE OF TWENTION: SECRETCHY CHIL LINES CORRESPONDENCE: 79 CORRESPONDENCE AUDHESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFERAY1PKEOKYSFLQNP 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPPRATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Rélease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,582
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.1%; Score 255; DB 3; L
ilarity 100.0%; Pred. No. 5.4e-29;
Conservative 0; Mismatches 0;
                         Halban, Philippe A.
No. 6110707mington, Karl D.
Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6C/028,427
ELING DATE: 15-0CT-1996
PRIOR APPLICATION LATA:
APPLICATION NUMBER: 08 (88/589,628
FILING DATE: 19-30N-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37.642
REFERENCE/DOCKEI NUMBER: UTSD:514
TELECOMMUNICATION INFORMATION:
TELEPAX: 512/418-3000
TELEFAX: 512/418-3000
INFORMATION FOR SED ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                              3: Arrold, White & Durkee
P.C. Box 4433
Newgard, Christopher B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-FOS/WS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 360 amino acids
amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                STREET: P.C. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas
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US-08-784-582-73
                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH:
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347.945 Millon cell updates/sec
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                                                                                                                                                                                    September 15, 2003, 12:03:35 ; Soarch time 20.5484 Seconds
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1 MEPTIPLSKLEDNAMLRAHR.....ORFSEAVIPKEGKYSFLONP
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2. /cgnt_6/ptocata//pubpaa/USC7_PUBCOMB.pop.*
3. /cgnt_6/ptocata//pubpaa/USC6_PUBCOMB.pop.*
4. /cgnt_6/ptocata//pubpaa/USC6_PUBCOMB.pop.*
5. /cgnt_6/ptocata//pubpaa/USC6_PUBCOMB.pop.*
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6. /cgnt_6/ptocata//pubpaa/USC6_PUBCOMB.pop.*
8. /cgnt_6/ptocata//pubpaa/USC6_PUBCOMB.pop.*
9. /cgnt_6/ptocata//pubpaa/USC9_PUBCOMB.pop.*
10. /cgnt_6/ptocata//pubpaa/USC9_PUBCOMB.pop.*
11. /cgnt_6/ptocata//pubpaa/USC9_PUBCOMB.pop.*
12. /cgnt_6/ptocata//pubpaa/USC9_PUBCOMB.pop.*
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/ogn2_6/prodata/1/pubpaa/US10_NBW_PUB.pop:*
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/cgn2_6/ptcdata/1/pubpaa/US10H_PUBCOMB.pep:*
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GenCere version 5.1.6
Copyright (c) 1993 - 2003 Compugen 188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541936 seqs, 145912426 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000060000
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                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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ALIGNMENTS

score by analysis of the total score distribution.

Score Match Length DB 15

Score Match Length DB 15

260 100.0 49 14 03-10-554-674.1 Sequence 1, Appl 260 100.0 107 14 03-10-554-674.2 Sequence 2, Appl 260 100.0 107 14 03-10-554-674.2 Sequence 2, Appl 255 98.1 191 12 03-10-454-774.7 Sequence 2, Appl 255 98.1 191 12 03-10-40-474.1 Sequence 1, Appl 255 98.1 191 12 03-10-40-474.1 Sequence 1, Appl 255 98.1 214 12 35-10-458-3 Sequence 1, Appl 255 98.1 214 12 35-10-458-3 Sequence 6, Appl 255 98.1 217 12 03-10-458-3 Sequence 6, Appl 255 98.1 217 12 03-10-458-3 Sequence 6, Appl 255 98.1 217 12 03-98-918-5 Sequence 6, Appl 269 95.8 217 10 03-09-893-688-2 Sequence 2, Appl 249 95.8 217 10 03-09-893-688-2 Sequence 4, Appl 249 95.8 217 10 03-09-894-408-4 Sequence 4, Appl 242 93.1 217 9 03-09-894-408-4 Sequence 4, Appl 243-688-4 Sequence 4, Appl 243-688-4 Sequence 4, Appl 243-688-4 Sequence 4, Appl 244 93.1 217 9 03-09-894-408-4 Sequence 4, Appl 244 93.1 217 9 03-09-894-408-4 Sequence 4, Appl 244 93.1 217 9 03-09-894-408-4 Sequence 6, Appl 244 93.1 217 9 03-09-894-4 Sequence 6, Appl 244 93-4 Sequen

. У IYPE: amino acid

Sequence 12, Appliant Sequence 3, Appliant Sequence 13, Appliant Sequence 14, Appliant Sequence 14, Appliant Sequence 14, Appliant Sequence 17, Appliant Sequence 19, Appliant Sequence 11, Appliant Sequence 11, Appliant Sequence 11, Appliant Sequence 12, Appliant Sequence 13, Appliant Sequence 14, Appliant Sequence 15, Appliant S	63 27, 27, 22, 22, 23,
US-09-824-260-12 US-09-850-887-3 US-10-153-207-2 US-10-153-207-2 US-10-153-207-2 US-10-153-207-3 US-09-876-478-2 US-09-876-478-2 US-09-876-478-3 US-09-876-478-7 US-09-876-478-7 US-09-876-478-7 US-09-876-478-7 US-09-876-478-7 US-09-876-478-7 US-09-876-478-7 US-10-191-879-10 US-10-191-879-12 US-10-191-879-12 US-10-191-879-12 US-10-191-879-13 US-10-100-679-61	S-10-100-679-6 S-10-036-869-2 S-10-036-869-2 S-10-140-293-1 S-10-140-293-2 S-10-140-293-2
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RESULT 1

(S-70-624-873-1)

S-70-624-873-1

S-70-624-874-12A1

S-70-624-874-12A1

GENERAL INFORMATION:

GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSER: TOwnsecd and Townsend and Grew LiP

STREET: TWO Embarcadero Center, Eighth Floor

CITY: San Francisco

STREET: TWO Embarcadero Center, Eighth Floor

CITY: San Francisco

CITY: San Francisco

COMPUTER: 1984

COMPUTER: 1987

COMPUTER: 1987

COMPUTER: 1887

COMPUTER: 1887

COMPUTER: 22-441-200

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 10/054,873

FILING DATE: 22-441-200

ATONESTATION NUMBER: WE 09/423,100

FILING DATE: 13-487-1998

APPLICATION NUMBER: WE 09/423,100

FILING DATE: 11-48-1998

APPLICATION NUMBER: WE 09/45

REFERENCE/DOCKET NUMBER: 46,946

REFERENCE/DOCKET NUMBER: 46,946

REFERENCE/CHARACTERISTICS:

LENGTH: 49 amino acids

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Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gan, Zhong Ru
IITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                     1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEOKYSFLGNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 260; DB 14; Length 49; Best Local Similarity 100.0%; Pred. No. 5.6e-28; Matches 49; Conservative 0; Mismatches C; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 260: DH 14: Length 92; Pred. No. 1.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.5, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: 18/10/054,873 FILING DATE: 22-Jan-2002 CLASSIFICATION: CUNNOWN>
PRIOR APPLICATION DATA: WO PCI/CN98/00052 FILING DATE: 3-MAR. 299 APPLICATION NUMBER: WO 90/423,160 FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DGS/MS-DGS
    TOPOLCGY: licear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-054-873-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10054879 Publication No. US20020164712At GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/10054873
; Publication No. US20020164712AL
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
STRANDEDNESS: <Unk,:Own>
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LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCUNTRY: USA
ZIP: 94:11:-3834
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US-10-054-873-6
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                                                                                                                                                                                                                                                                                                            RESULT 2
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Gaps
APPLICANT: Gan, Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !ITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                            COUNTRY: USA

ZIP: 9411:2384
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1RM PC COMPATIBLE
OPPROTER: 1RM PC COMPATIBLE
OFFATING SYSTEM: PC-DOS/MS-DOS
SCFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLF
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-090130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 260; DB 34;
100.0%; Pred. No. 1.4e-27;
Uive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10054873
Publication No. US20020164712A1
GENERAL INFORMATION:
APPLICANT: Gan, Zhong Ru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                                                                                                        CIIY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-054-873-6
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APPLICANT: COX 111, George N
APPLICANT: Bolder Biotechhology, Inc.
APPLICANT: Bolder Biotechhology, Inc.
TILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REPERENCE: 4152-2-673
CUPRENT APPLICATION NUMBER: US/10/400,377
CUPRENT PAPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ 10 NOS: 41
SOFTWARE: Palentin Vor: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                    | FPT | PUSEL FOR MALKAHKLHOLAFDTYQEPEBAY I PKEGKYSFLONF 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FPTIPLSRLFONAMLRAHRLHQLAFDTYGEFEEAYIPKEQKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPTIPLSKLFUNAMLRAHRLHQLAFDTYQEFEEAYIPKFQKYSFLQNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%: Pred. No. 1.3e-26;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT PILIGATION NUMBER: US/10/153,207
CURRENT FILING DATE: 2002-05-22
PRIOR PROPICCATION NUMBER: 08/479,894
PRIOR FILING DATE: 1955-06-07
PRIOR FILING DATE: 1959-06-07
PRIOR PAPILICATION NUMBER: 08/190,723
PRIOR FILING DATE: 1994-02-02
PRIOR FILING DATE: 1992-01-13
PRIOR FILING DATE: 1992-01-13
PRIOR FILING DATE: 1992-04-27
                                                                                                                                                                                                                                                                     Sequence 1. Application US/10153207
PUBLICATION US. US20830153063A1
APPLICANT: James A. Wells
APPLICANT: Brian C. Cunningham
APPLICANT: Brian C. Cunningham
APPLICANT: GROWTH HORMONE VARIANTS
FILE REFERENCE: 669.12-07-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICK APPLICATION NUMBER: 07/428,066
PRICK FILING DATE: 1969-16-26
PRICK APPLICATION NUMBER: 07/264,611
PRICK APPLICATION NUMBER: 07/264,611
PRICK FILING DATE: 1988-10 28
NUMBER OF SEQ ID NOS: 26
SUFFRARE: FASLES for Kindows Version 4.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRI
ORGANISM: Homo Sapiens
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US-10-406-377-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL
TITLE OF INVENTION: RETOMBINANT FUSION PROTEINS TO GROWTH BORRONE
ALICENOME AND SERUM ALREMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Street
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CORRESPONDENCE FINNEDAM, HENDERSON, FARABOW, GARRETT & DUNNER, STREET: 1300 I Street, NW CITY: Washington SIATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

21F: 20005-31;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC DCOS/MS-DCS
OFTWARE: PatentI: Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DAIA:
APPLICATION NUBEF: US/09/984,6:0
FILING DATE: 21-Ms y-2002
PRIOR APPLICATION DAIA:
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Best Local Similarity 100.0%; Prod. No. 2.1e-27;
Matches 49; Conservative 0: Mismatches 0: Indels 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPTIPLSRIEDNAMLRAHRIBQLAFOTYCEFEBAYIPKBOKYSFLONP 43
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                            APPLICATION NUMBER: WC PCI/CN98/00052
FILING DATE: 31-MAR:1998
APPLICATION NUMBER: WS 69/423,100
FILING DATE: 11-DEG-2000
ATTORNEY/AGENT INFORMATION:
NAME: MYCTOFT, FYARK J
RGGISTRATION NUMBER: 46,946
BERERANDES/OGCKET NUMBER: 020167-960170958
INFORMATION FOR SEQ 11 NO: 7:
SEQUENCE CHRRATERISISS:
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FILLING DATE: 25-JUN-1998
APPLICATION NUMBER: PCT/GB96/03164
FILLING DATE: 19-DEC-1996
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
SECTENCE DESCRIPTION: SEQ ID NO: 23:
US-09-984-010-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/0994010
Publication No. US20030164578A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 191 amino acids
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPCLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sato, Selj:
APPLICANT: Higashikuni, Naoniko
APPLICANT: Higashikuni, Naoniko
APPLICANT: Higashikuni, Naoniko
APPLICANT: Higashikuni, Nasaaki
IIIIE GE INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
IIIIE GE INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
IIIIE GE INVENTION: DNAS ENCODING NEW FUSION PROTEINS DANS
CURRENT PRILIAG DATE: 1999-03-26
EARLIER APPLICATION NUMBER: JP10-87339/1998
EARLIER APPLICATION NUMBER: JP10-87339/1998
SARLIER FILING DATE: 1996-03-31
NUMBER OF SEO ID NOS: 66
SOSTWARE: PARENTIN VOR: 2.0
SOSTWARE: PARENTIN VOR: 2.0
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                                                                                                                          Sequence 9. Application US/09929918
Fatest No. 68200000667841
Fatest No. 6820000067841
Fatest Nordon Slavehonko, 1770 14
FAPLICANT: Slavehonko, 1770 14
FAPLICANT: Slavehonko, 1770 14
FATES FATEST NORTON: PHAGE-DEPENDENT SUPER PRODUCTION OF TITLE CF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES FILE REFERENCE: PHAGE 0064
CURRENT APPLICATION NUMBER: US/09/929,918
FORRENT APPLICATION NUMBER: US/09/929,918
FORRENT APPLICATION NUMBER: 05/01-08-15
FORRENT APPLICATION NUMBER: 05/01-08-15
FORRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 FPTIPLSRIFDNAMIRAHRLHQLAFDTYQEFEEAYIPKEÇKYSFLQNP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 245;
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        24 FPTIPLSRLFUNAMURAHRUHQLAFN/YQBFRBAYIPKEQKYSFLONP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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llarity 100.0%; Pred. No. 1.7e-26;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%; Score 255; DB 9; I
100.0%; Pred. No. 1.5e-26;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 66, Application US/09280030A Patent No. US25010021515A1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Bost Local Similarity 100.(
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-09-529-918-9
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Les 48; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FESULT 11
US-09-280-030-66
                                                                                     RESULT 10
T8-69-929-918-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 217
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                                                                                                                                                      Sequence 1. Application US/12400789
| Publication No. US2603015685541
| GENERAL INFORMATION
| GENERAL INFORMATION
| APPLICANT: Cox III. George N
| APPLICANT: Cox III. George N
| TITLE OF INFORMATION
| TITLE OF INFORMATION
| TITLE OF INFORMATION
| TITLE OF INFORMATION NUMBER: US/10/460.708
| CURRENT FILING DAIE: 2003-03-25
| PRIOR FILING DAIE: 2000-01-14
| PRIOR FILING DAIE: 1997-00-14
| PRIOR FILING DAIE: 1997-07-14
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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* FPTIPLSKLEDKAMIKAHRINGSAROTYGERBAYIPKNOKYSPIGNE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sength 191;
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100.0%; Pred. No. 1.3e-26;
cive C; Mismatches 0;
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98.1%; Score 255; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 48; Conservative 0; Mismatches 0;
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TITLE OF INVENTION:
TITLE OF INVENTION: GROWTH HORMONE VARIANTS:
FILE REFERENCE: 609.12-CS-CY
CURRENT APPLICATION NUMBER: US/TU/153,207
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US/TU/153,207
PRIOR FILING DATE: 1965-66-37
PRIOR FILING DATE: 1967-66-37
PRIOR FILING DATE: 1995-06-37
PRIOR FILING DATE: 1995-06-37
PRIOR FILING DATE: 1995-07-96
PRIOR PELING DATE: 1992-04-37
PRIOR FILING DATE: 1992-04-37
PRIOR FILING DATE: 1999-10-26
PRIOR PLING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1989-10-26
PRIOR FILING DATE: 1986-10-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ fOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Sequence 6, Application US/10153207
// Publication No. US20030153003A1
// GENERAL INFORMATION:
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Matches 48; Conservative
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CRGANISM: Home sapiens
US-10-406-708-1
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ORGANISM: HOMG Sapleds
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US-10-153-207-6
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APPLICANT: PROCTER, ANNIE M.
APPLICANT: COOPER, JOHN
APPLICANT: GRESORY, JOHN
APPLICANT: MILLAR, DAVID S.
TILLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
TILLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
FILE REPERENCE WORMS
CURRENT APPLICATION NUMBER: US/09/853,688
CURRENT FILING DAIE: 2001-05-14
SUMBER OF SEC ID NOS: 66
SOFTWARE: PALCHIN VOF: 2.1
SEC ID NO 4
SEC ID NO 5
SEC I
                                          Sequence 16, Application US/09804469A
Patent No. US20020155100A1
GENERAL THORNATION:
APPLICANT: KIEFFER, ITMOREY J.
APPLICANT: CHEUNG, ANTHONY T.
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
TILE OF INVENTION: EXPRESSION IN GUT
SILE RFERENCE: 029996/027 8721
CURRENT APPLICATION NUMBER: US/C9/604,409A
CURRENT FILING DATE: 2601-03-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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Matches 46; Conservative
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OKGANISM: Homo sapiens
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US-09-853-688-4
      US-09-804-409A-16
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ES-09-853-688-4
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                              Sequence 2, Application 35/09E51688

Patent No. US20020081605A1

GENERAL INFORMATION:
APPLICANT: GRECKHYTON:
APPLICANT: GRECKHY JCHN
APPLICANT: GRECKHY JCHN
APPLICANT: MILLAK JCHN
APPLICANT: METHOD FCH RETECTING GROWTH HORSYNE IN FIRE FFILE METHORS AND THEFT HISTONS AND THE HISTONS AND THEFT HISTONS AND THEFT HISTONS AND THE HISTONS AND THEFT HISTONS AND THE HISTONS AND THEFT HISTONS AND THE H
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1.vc C; Mismatches D; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 97,99
Matches 47; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-569-748C-4
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US-09-853-688-2
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OM protein - protein search, using sw model

Septembor 15, 2003, 11:56:45; Search time 8:07885 Seronds (Without alignments) 583.284 Million cell updates/sec Run on:

US-69-423-100-1 260 1 MEPTIPLSRLFDNAMLRAHR..... Title: Perfect score: Sequence:

Scoring table:

....OBFERAYIPKRDXYSFLONP 49

283338 seqs, 96158682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

383308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200030366)

Post-processing: Minimum Match 08
Maximum Match 190*
Listina first 45 summaries

P.TR_76:* Database

pirl:*
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Pred. No. is the number of results predicted by charce to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sescription	somafotropia 1 pro	:	somatotropin 2 pre	somatotropin 2 pre	Na:	chorionic somatoma	scmatotropin - :he	chorionic somatoma	choriomammotrepin	choriczammotropin	chorianammetropin	somatotropin precu		٠	somatotropin - Alr	somatetropia - Arr	Somatetropin pred.	somatcing and store	Somatotropin propi	somatofropin predu	.:	socatotropic precs	sometofropic precu	soratotropic - alp	sometotropic precu	somatotropin - are	soratotropin - sel	somatofropin - Pus	somatotropin precu
6	STHE	:67410	STHUY	STHUV2	157408	153267	I67411	I67409	A26449	CHUC	E32435	STMS	PN0140	STHO	CK0219	350429	STRI	STPG	:46145	849483	B49159			A61584	JC15:4			821750	
Length J3	1		2:7 1																						216 2				
% Ouery Match 1	98.1	98.1	87.7		81.9							62.1								61.3	*		60.2	8.65	57.7	56.9	56.2	55.4	55.4
Score	255	255	228	228	213	213	202	203	197	197	197	161.5	160.5	159.5	159.5	159.5	159.5	159.5	159.5	159.5	159.5	159.5	156.5	155.5	150	148	146	144	144
Result No.	1	7	m	ক	Ω	9	7	83	6	10	11	12	13	14	15	16	17	18	51	20	21	22	23	24	25	26	27	28	29

somatotropin precu	somatotropin precu	somatotropin precu	somatotropin - dom	somatotropin precu	somatotropin - bul	somatotropin - bul	scmatctropin - bow	somatotropin precu	choriomammotropin-	somatotropin - blu	EST/beta-Sal mutan	growth hormone - g	growth hormone II	growth hormone I p	somatotropin precu
STBC	STSH	STGT	S32682	S04929	A56916	151188	151250	JS0037	B32435	A60623	167761	IS1114	869263	S69262	SC2764
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217	2:7	217	223	2:6	06.	215	195	215	199	183	8.3	200	210	210	210
54.8	54.8	54.8	54.8	53.8	50.8	50.8	49.2	49.2	46.9	44.6	37.3	37.3	(2) (2)	33.5	33.5
	142.5 54.8						126 49.2				98.5 37.9	97 37.3	87 33.5	87 33.5	87 33.5

ALIGNMENTS

Numerotropin 1 precursor (validated) - human Nichternate names; growth hormone 1, hähln, pitultary somatotropin Nichternate names; growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1, somatots; Homo Sapiens (man) Cibate; 24 Apr. 1984 Requence, revision 10-Feb-1995 #text_change 08-Dec-2000 Cibate; 24 Apr. 1984 Requence, revision 10-Feb-1995 #text_change 08-Dec-2000 Cibates of the second of	1, s
A:Attenfact names: growth hormone 1: nam'n; piculidary somatortopin names: growth hormone 5K peptide; somatotropin i. Long form; somatotropin C.Species: Homo saplens (man; revision 10-Feb-1995 *text_change 08-Dec-2000 C.Species: Apr-1984 *sequence_revision 10-Feb-1995 *text_change 08-Dec-2000 C.Accession: A9373: A32435; A93447; A92447; A90051; A93397; A93785; A91764; A R.Donoto, E.M.; Moore, D.D.; Scodman, H.M. Norte, D.D.; Scodman, H.M. Nichele Accession and Anthrope of Annamed Control of Annamed Cont	1, 8
C.Species: Homo Sapiens (mar.)	
Cloate: 24 Apr.1984 #Asquebro_revision 10-Feb.1995 #text_change 08-Dec-2000	
RIDONGSO, F.M.; Moore, D.D.; Scodinan, H.M.; Nicheller, C.C.; F.M.; Moore, D.D.; Scodinan, H.M.; Nicheller, A.S.; S. 3715/2-3730, 1981.	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
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A:Accession: A93731	
A:Molecule type: DNA	
A:Residues: 1-217 <den></den>	
A:Cross-references: GB:V00520	
A)Note: the 20K short form sometotropin lacks residues 58-72 (32-45 in the act	ive n
Nichter, E.H. 1404, 1.0.1 Switch, Orn.; Barkera-Saldana, B.B.; Cerimas, P.E.; Seedun Genomics 4, 479-487, 1989	מבות
Assisted the human growth hormone locus: nucleotide sequence, biology, and evolution	lutio
A) Reference number: A32435; MUID:89307277; PMID:2744760	
A: Accession: A32435	
A:Molecule type: DNA	
A:Cross-relerances: GB:C030/1; NID:G183148; FIDN:AAAD2049.1; FID:G183149	
NETROSKAM, P. NOUGEROU, F. NOUGEROU, P. NOUG	
A:Title: Kiecular cloning and nucleotide sequence of the human growth hormone	stru
A; Reference number: A93694; MUID:80034477; PMID:386281	
A; Accession: A93694	
A) WOLGGOLG LYPE - BRNA N-DOCK - 1-217 - VDOCK	
A Newstrates - 1 1 1 / A NOS. A Norses - rationals - OR VOOS. 9	
A.Note: 35-Pro was also found	
R.Martial, J.A., Hallewell, R.A., Baxter, J.D., Goodman, H.M.	
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A.Title: Human growth hormone: complementary DNA cloning and expression in backing and expression in backing the complementary with a footback of the complementary with a footback of the complementary with a footback of the complementary with the complementary of the complementary of the complementary with the complementary of the complementar	bacteria
A. ACCESSION - AGAZA?	
A;Molecule type: mRNA	
A:Residues: 1-217 <mar></mar>	
Rilli, C.H.; Dixon, J.S.; Liu, W.K.	
Arch. Blochem. Bloppys. 13, 70-91, 1969	
Allite: Human pirititaty growit formone: XIX, ine primary structure of the normone analysis of the normone. Also assessed of the solution of t	none.
A. Matandrado Januara a Novaso Halling Consolidado de Maria Consolidado de Alemanda de Maria	
R. M. S. C. H.; Dixon, J. S.	
Arch. Biochem. Biophys. 146, 233-236, 1971	
	ormon
A:Reference number: A90051: MUID:72143935; PMID:5144027	
A; Argession: A90051	
A; Molecule type: protein	

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27-94:96-217 <1.10>

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scmatotropin 2 precursor - human 2. growth hormone variant, hGii-V; placental somato Nichternate names: growth hormone 2. growth hormone variant, hGii-V; placental somatotropin. 2. long splice form; somatotropin 2, short splice form CiSpecies: Homo sapiens (man) (CiSpecies: Homo sapiens (man) (CiSpecies: Homo sapiens (man) (CiSpecies: Homo sapiens (man) (Man
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in somatotrophic cells
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Alutrons 4/1: 57/3: 97/3: 152/3
Cisupertably; probactin
Cisupertably; probactin
Cisupertably; probactin
Cisupertably; probactin
Fil-26/Domain: Signal sequence #status predicted <SIG>Fil-26/Domain: Signal sequence #status predicted <SIG>Fil-26/Domain: Signal sequence #status predicted <SIG>Fil-26/Product: growth lorrance 5K peptide #status experimental <SCI>Fil-27-57/57-217/Product: somatotropin 1, short form #status experimental <SOS>Fil-79-191,206-215/Disulfide bonds: #status experimental
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A.Mesidues: 1-217 <RES>
A.Cross-references: GBL116556; NID:9293114; PIDN:AAA18842.1; PID:9
R:Li. C.H.: Chung, D.: Lahm, H.W.; Stein, S.
R:Cri. Bicchem. Biopiys. 245, 287-291, 1986
A:Ti:Le: The primary structure of monkey pituitary growth hormone.
A:Reference number: A05094; MUID:86129460; PMID:3080959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 PPIIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 255; DB 1; Length 217; Pred. No. 2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
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A.Rote: the morkey species is not identified in the reference service 125, 681-884, 1957
A.Title: Proparation of growth hormone from pituitaries of mar A.Reference number: A44794
A.Contents: amoutanion; identification of source organism
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Contents the gone for this barmone is transcribed only in Comments About 90% of someternopin is the 22K long form
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:ive 0; Mismatches 0
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nes 48; Conservative 0; Mismatches
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A.Cross-references: GDB:113982; OMIM:139250
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A:Residues: 27-99,'Q',103
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167410
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Amorecal type: Table May Fig. 1990
Antitie: Identification of the aspartimide structure is a proviously-reported pyrine.
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A) Residues: 46-77,33-86 c.EW>
B) Residues: 46-77,33-86 c.EW>
B) Chem. 256, 2395-240, 1981
A) File: The 29,006 molecular weight variant of human growth hormone. Proparation and so A) File: The 29,006 molecular weight variant of human growth hormone. Proparation and so A) Feforence number: A92311; MUID: 8117361; PMID: 7462247
A) Contents: somatotropin, 20K short variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in Productin and Carcinogenesis, Proc. Fourth Tenevis Workshop Productin, Griffiths, K., A; Title: The chemistry of the human lactogenic hormones.

A; Reference number: A4427
A; Contents: annotation; somatotropin revision;
B; Bewley, T.A.; Dixon, J.S.; Li, C.H.
A; Dixon, J.S.; Li, C.H.
A; Dixon, J.S.; Li, C.H.
A; Title: Sequence comparison of human pituitary growth hormone, human choricule somatoms
A; Reference number: A91764; MJID:73092028; PMID:4675454
                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 27-51 kNIA>
R;Niall, H.D.; Hodau, M.L.; Sauer, R.; Rosenblum, 1.Y.; Greenwood, F.C.
Proc. Natl. Acad. Sci. U.S.A. 68, 856-869, 1971
A;Itle: Sequences of pituitary and placental lactificatic and growth homenes: evolution
A;Reference number: A93778; MUID:71153968; PMID:5229524
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A,Reference number: A61466
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecules: 1-26 cRES>
A;Cross-references: GB:M14398; NID;g183158; PIDN:AAA52554.1; PiD:g183159
                                                                                                                                                 Ajfitle: Revised primary structure for human growth bounder. A;Reference number: A3387; KUID 71139765; PMID:5279046
A;Accession: A93397
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A)Residues: 27-57;73-79 <CHA>
R;Singh, R:N.P.: Seavey, B.K.: Ltwis, L.J.: Lewis, U.J.
J. Protein Chem. 2, 425-435, 1983
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A;Molecule type: protein
A;Residucs: 119-120;157-159 <N12>
R;Niall, H.D.
                                                                                                          Nature New Biol. 230, 90-91, 197.
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Gaps

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Clacression: 157408
RiGolos, 1.G.: Durning, M.: Fisher, J.M.; Fowler, P.D.
Endoctinology 133, 1744-1752, 1997
A)Title: Gloring of Iour growth hormone/chorionic somatomammotropin-related complem
A:Reference number: 153267; MUID:94008724; PMID:8404617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rigoles, T.G.: Durning, M.: Fisher, J.M.; Fowler, P.D.
Endostinology 135, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomammotropin-related complem A;Reference number: 153257; MJID:940003224; PMID:8404617
A;Reference number: 153257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chorionic scratomarmotropin-2 - rhesus macaque (fragment)
S:Species: Manaca mulatta (rhesus macaque)
S:Sato: 31-May-1996 #sequenco_revision 31-May-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Macaca mulatta (Thesus macaque)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-212 <RES>
A,Cross-references: GR:L1655%: NID:9293110; PIDN:AAA18840.1; PID:9293111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: GB:016552; NID:9293108; PIDN:AAA18839.1; PID:9293109
0:Superfamily: prolactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.9%; Score 213; DB 2; Length 212; 78.7%; Pred. No. 3.46-19; 1ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PTIPLSRLFDNAMLRAHKLHQLAFDTYQEFEEAYIPKSQKYSFLONP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 PSVPLSRLFDHAMIQAHREHQLAFDTYQEFEEAYIPKEKKHSLMENP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 PSVPLSRLFDHAMIOAHRLHQLAFDTYQEFEEAYIPKEKKHSLMENP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Accession: 167408
A.Status: preliminary: translated from GB/EMBL/DDBJ
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Best Local Similarity 78.79
The American 37, Conservative
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Matches 37; Conservative
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A; Residues: 1-217 <RES>
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    A;Accession: A28072
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Astrocession: 12.114
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Astrocession: A60711
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STHUVZ
SOMBLOCKTOPID 2 PRECURSOR, Splice form 2 - human
N'Alternate names: growth hormone variant-2; placental somatotropid norm 2
N'Alternate names: growth hormone variant-2; placental somatotropid norm 2
C;Species: Homo Sapiens (man)
C;Date: 30-Sep-1969 #sequence_revision 10-Fcl-1955 #text_change 02-Sep-1567
C;Date: 30-Sep-1969 #sequence_revision 10-Fcl-1955 #text_change 02-Sep-1567
R;Cooke, N.E.: Ray, J.: Emery, J.G.: Liebhaber, S.A.
3. Biol. Chan, 263, 9601-9066, 2388
A;Title: Two distinct species of human growth Horron-variant mRNA in the human placental A;Reference number: A92725: MUID:88243759; PMID:3379657
                        A/Title: The human growth normone locus: nucleotide sequence, biology, and evolution.
A/Reference numbor: A42435; M/HU:89307277; PM/HU:2744760
A/Accession: D12435
A/Accession: D12435
A/Residucs: 1-217 < CHED
A/Residucs: 1-217 < CHED
A/CROSS - references: GEN-03071; NID:9183148; PIDN:AAA52832 I; PID:9183152
B/COOKA, N.E., Ray, J.; Emery, G.G.; Glebhaber: S.A.
A/Title: Two distinct species of human growth hormone-variant mRNA in the human placental A/Reference number: A92725; MULL:89243769; PM/HD:3374687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA 1, 239-249, 1982
AJTILE: The busan growth hormore gone family: Durchedide sequences show resent diversor
A)Reference number: A01511: MULD: 83182010; PMID: 71-9009
A/Accession: A01511
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A:Residues: 1-44, PV, 36-217 -SBE.
R:Igout. A. Scippo. M.L.: Frankone. F.: Hennen. G.
Arch. Int. A-) Scippo. M.L.: Frankone. F.: 1998
Arch. Int. A-) Scippo. M.L.: Frankone. F.: 1998
A.Fittle: Clocking and n.cinotide sequence of piacental MSH-V CDNA.
A:Reference number: 152104; MGID:89024984; FMID:246005C
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Genomics 4, 479-497, 1989
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A:Residues: 1-217 <000>
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A.Accession: A94427
A.Molecule type: protein
A.Residues: 27-217 <MTA>
A.Residues: 27-217 <MTA>
A.Residues: 20-217 <MTA>
A.Residues: 20-217 <MTA>
B.R. A.Residues: 19-205. 1991
Blochem. Soc. Trans. 19, 265, 1991
A.Title: Catechol-O-methyltransferase from human placenta: purification and some pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: mRNA
A:Residues: 1-217 <GOO>
R:Tanaka, M.; Masuda, N.; Watahiki, M.; Yamakawa, M.; Shimizu, K.; Nagai, J.; Nakas
B:Chemen. Int. 16, 287-292, 1988
B:Title: cDNA cioning of human chorionic somatomammotropin-1 mRNA whose transcription
A:Reference number: 152342; MUID:88209096; PMID:2835050
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A.Residues: 1-3 <TAN>
A.Cross-references: 08:M35419; MID:9506822
A.Cross-references: 08:M35419; MID:9506822
A.Cross-references: 08:M35419; MID:9506822
A.Title: Primary structure of the NH-2-terminal extra piece of the precursor to hum. A.Reference number: A93833; MJID:80034970; PMID:291043
A.Accession: A93833
A.Molecule type: protein
A.Residues: 1,3-25 <SRBC
A.Residues: 1,3-25 <SRBC
A.Residues: A.S. A.Residues
A.Residues: A.Residues
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A)Residues: 27-217 <11C>
A)Experimental source: plucenta
B)Nically H.D.
In Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths
A)Title: The chemistry of the human lactogenic hormones.
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A:Acression: A93192
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k;Goodman, H.M.; DeNoto, F.; Fiddes, J.C.; Hallewell, R.A.; Page, G.S.; Smith, S
in Mobilization and Reassembly of Genetic Information, Scott, W.A.; Werner, R.,
A;Reference number: A94422
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A:Residues: 50-27 * *SHI>
A:Experimental source: placenta
R:Li, c.H.; pixon, J.S.; Chung, D.
A:Arci, Bixoficen, alsophys, 155, 95-110, 1973
A:Title: Amino acid sequence of human chorionic somatomammolropin.
A:Reference number: A90054; MJTD:73201971; PMID:4712450
                                                                                                                                                               4 TIPOSKLFONAMURAHROHAPOTYOEFEBAYIPKEQKYSFLGN 48
                                                                                                                                                                                                                  29 TVPLSRLFDHAMLQAHRAHQLAIDTYQEFEETYIPKDGKYSFLHD 73
                                             Indes
Pred. No. 3.40
): Mismatches
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A:Status: translated from GB/EMBL/DDBJ
becal Similarity 80.6
es 36: Conservative
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A:Residues: 1-217 <CHE>
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                                             Matches
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Nationate names growth horizon
Nationate names growth horizon
Nationate names growth horizon
Nationate names growth horizon
Nationate names growth for theses menupe)
C. Species: Macaca mulatia (Theses menupe)
C. Species: May 1996 Seguence_revision 1 - Ray-1946 Etext change [6-10:1-1997]
C. Accession: 15741
R. Golos, T. G.; Dunning, M.: Fishi, J.M., Fowler, P.D.
Endocrinology 133, 1744-1752, 1933
A. Title: Cloning of four growth Gorrone/chorionic scharomanmotrapin related wespementally Accession: 16741
A. Secatus: proliminary; translated from GB/EMBL/DDMJ
A. Scatus: proliminary; translated from GB/EMBL/DDMJ
A. Scatus: proliminary; translated from GB/EMBL/DDMJ
A. Scatus: growth mRNA
A. Rossiues: 1-217 GRES
A. Cross references: GB-L16555; NID:9293116; PIDN:AAAZGLW0.1; PID:9299117
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Cyspecies: Macaca mulatta (rhosus macaque)
Cyspecies: Macaca mulatta (rhosus macaque)
Cyspecies: Macaca mulatta (rhosus macaque)
Cyspecies: 1-May-1996 #sequence_rewision 31-May-1996 #mext_change [6-Jui-1999
Cyaccession: 167409
BrGolos, T.G.: Durning, M.: Fisher, J.M.; Fowler, F.D.
BrGolos, T.G.: Durning, M.: Fisher, J.M.; Fowler, F.D.
Argolos, T.G.: Durning, M.: Fisher, J.M.; Fowler, F.D.
Argolos, T.G.: Durning, M.: Fisher, J.M.; Fowler, F.D.
Argologic, 1001 Goar growth hormone/chorical somatomamnotropin-related complementar
Argologic, 1001 Goar growth hormone/chorical complementary
Argologic
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CySpecies: Homo sapieus (man)
CySpecies: Abdus 3884 486quence_revision 30-Jun 1988 #text_change 28 ont-1995
CyScession: A55449
Rylitt, H.; Kimelnan, J.; Birnhaum, M.C.; Chen, B.Y.; Sceburg, P.H.; Ekethandt, M.C.; Bu
DNA 6, 59-70, 1987
Alitte: The human growth hormone gene locus: structure, evolution, and allelin variation
A.Reference number: A25449; MUID 87161235; PKID: 80:0680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ċ
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Csuperfamily: prodactive productsd <813*
F:1-26/Domain: signal sequence *status productsd <813*
F:1-215/Product: chorioxammouropin, hCS-3 allele *status predicted <857*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 FPIIPLSWLFNIAVFRAHALAKLAFOTYPKFEMAYIPKEUKYSFLANP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 PSVPI,SKLFDNIMKÇAHRLIQLAFDTYQEPEKTYTPKEKKESI,MSNP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.8%; Score 205; DB 2; Length 217; 79.2%; Fred. No. 3.56-18; Live 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sength 215;
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Pred. No. 1.1e-17:
8: Mismatches 4
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74.58;
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Best Local Similarity 79.28
Find 38: Conservative
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Best Local Similarity 74.55
Matches 35; Conservative
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Accession: B2991

R.Linzer, D.1.H.: Tolamattes, F.

R.Linzer, Chem. 260, 9574-9579, 1995
A.Tittle: Monectide Sequence of mouse prolactin and growth hormone mRNAs and expres
A.Reference number: A92548, MJID:85261358, PMID:2991252
A.Accession: B2991
A.Molecule type: mRNA
A.References: GB:X02891; GB:K03232; NID:951367; PIDN:CAA26650.1; PID:q5:068
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C:Species: Balaenoptora borealis (sei whale)
C:Species: Balaenoptora borealis (sei whale)
C:Date: 07-May-1993 #sequence_revision 07-May-1999
C:Accession: PN0140
R:Yudaev, N.A.; Pankov, Y.A.; Bulatov, A.A.; Osipova, T.A.
Biokhimia 47, 1059-1669, 1982
A:Title: Amino acid sequence of seiwhale somatotropin.
A:Reference number: PN0140; MJD:83000569; PMID:7115813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Mus musculus (house mouse)
C:Date: 3C-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 28-May-1999
    A;Molecule type: DNA
A:Rosiduos: 1:217 <CHE>
A:Rosiduos: 1:217 <CHE>
C:Genetics: GB:J03071; NID:g183148; PIDN:AAA52553.1; PID:g183153
C:Genetics: A:Gene: GDB:CSH2
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TIPLSRIFDNAMIRAHRCHQLAFDTYQEFEEAYIPKEQKYSFLQN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 TVPLSRLFDGAMLQAHRAHQLAIDIYQEFSETYIPKDQKYSFLHD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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C.Koywords: anterior pitulitary; growth factor; hormone
Filze/Domain: signal sequence *status predicted <SIG>
Filze/2/26/Product: somatorropin *status predicted <SIG>
Filze/2/26/Product: somatorropin *status predicted <SIN
File:189,206-214/Pisulfide bonds: *status predicted
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Pred. No. 1.1e-12;
6; Mismatches 8;
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itarity 58.1%; Pred. No. 9.4e-13;
Conservative 5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 197; DB 2;
80.0%; Pred. No. 3.5e-17;
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C:Superfamily: prolactin
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                                                                                                                                                                                                                                  GDB:119813; OMIM:118820
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N:Alternate names: growth hormone
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Hest Local Similarity 80.0%
Marches 36, Conservative
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Best Local Similarity 68.1
Matches 32, Conservative
                                                                                                                                                                                                                              A)Cross-references: ODB:1198
A;Map position: 17q22-17q24
C;Superfamily: prolactin
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Best Local Similarity
Matches 32, Conserve
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A;Residues: 1-190 <YUD>
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                                                                                                                                                            Aprices chorionammotropin apparently copiritied with placental catechel-oracliginansies (Signerwood, L.M.) Eanderger, S. McLaurin, W.D., Lanner, M. Aprices chorionammotropin apparently copiritied with placental catechel-oracliginansies (Signerwood, L.M.) Eandercaer, S. McLaurin, W.D., Lanner, M. Aprices chorional sequence of human placental lactoqua. Aprocessie annotation (M.) Processies (M.) Pr
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S.C.Accession: E32435
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S.C.Accession: B32435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A:Rosidues: 160-217 - CREZ>
A:Cross-references: GB:M25118; WID:q181124; PiEN:AAA35721.1; PTE:g141125
C;Genetics:
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A,Introns: 4/1; 57/3: 97/3; 152/4
C,Superfamily: prolactin
C,Keywords: hormone; procenta
C,Keywords: hormone; procenta
F,1-66/Domain: signal sequence "status experimental <STG>F;27-217/Product: choricmammotropin A #status experimental <MAT:
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A;Reference number: A61283; MUID:91244006; PMID:2037148
A;Accession: A61283
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Pred. No. 3.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: translated from GB/EMBL/DDBJ
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80.0%;
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                                                                                         A; Molecule type: protein
A; Residues: 27-46 <NIC>
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Matches 36; Conserv
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                                                                                                                                         Residues:
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2 FPIIPLSKLFUNAMLRAHRLHQLAFDIYQEFEBAYIFKEOKYSFLQN
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Job time : 9.07885
        7
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Nalterbate names: growth hormore
Copecies: Edguas caballus (domestic horse)
Romession: A91772. A91395: A9236; A9444, 136
Romession: A91772. A91395: A9376; A7444, 136
A71141e: Primary structure of equine growth hormore.
A.Rocession: A91772. Molic 77005410; PMID:96515.
A.Rocession: A91395
A.Rocession: A91395
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N.Altornate names growth hormone
C.Species. Loxodonta africana (African elephant)
C.Date: 03-Muq-1592 Sequence-ferision 03-Auq-1992 tiext_change [Sence is not chartered on JK0219
R.Hulmes, J.D.: Niedel, M.C.: Li, C.H.: Pan, Y.C.H.
Int. J. Pept. Protein Res. 33, 346-372, 1363
A.Title: Primary structure of eliphant growth hormone.
A.Reference namber: JR0219
A.Reference namber: JR0219
A.Residues: JR0219
A.Residues: 1-190 cHUL.
A.Residues: 1-190 cHUL.
A.Residues: 1-190 cHUL.
A.Residues: protein
B.J.-190/Product: somatotropin *status experimental cMAT>
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llarity 68.1%; Pred. No. 1.4e-12;
Conservative 6; Mismatches 8; Indels 1.
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- protein search, using sw model OM protein September 15, 2003, 11:54:00 | Search time 4.56631 Seconds (without alignments) 504:633 Million cell appartes/sec Run of:

08-09-423-100-1 260 Title: Perfect score:

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BLOSHM62 Gapop 10.0 / Gapext, 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match (% Kaximum Match 100% Listing first 45 summaries

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SOMA_SHEEP	SOMA_STRCA	SOMA_CRCNO	SOMA_ANAPI.	SOMA_BUBBU	SOMA_RANCA	SOMA_LEPOS	SOMA_XENLA	SOMA_PRIGL	SOMA_PROAN	SOMA_BUFMA	SOMB_XENLA
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POL241; 014405; 016531; C9HBZ1; Q9UKJ7; U9UNL5;
21-JJL 1986 (Rel. 01, Greated)
A. MART-1992 (Rel. 21, Last sequence update)
15.SEP-2003 (Rel. 22, Last annotation update)
Somatotropin prevarsor (Growth hormone) (GH-N) (Pitmitary growth hormone) (Growth hormone);
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MEDITINE-79203223; PubMed-374496;
Martial J.A., Hallewell R.A., Baxter J.D., Goodman H.W.;
"Human growth hormome: complementary DNA cloning and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REDIINE-89307277; PubMed=2744760;
Chon F.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A.,
Gelinas R.E., Seeburg P.H.;
"The human growth hormore locus: nucleotide sequence, biology, and
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Denoto F.M., Moore D.D. Goodman H.M.:
"Human growt: hormone DNA sequence and mRNA structure: possible
                                                                                                                                                                                                                                                                                                                                                                                                  Edkaryola, Metazoa: Chordata, Craniata; Vertebrata, Euteleostomi;
Kammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeburg P.H.; "The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone.";
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TISSUE=Pituitary.
Gu J., Hunny O.-H., Li N., Xu S.-H., Han Z.-G., Fu G., Chen Z.;
A novel gene expressed in hunan pituitary.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alternative splicing.";
Nucleic Acids Res. 9:3719-3730(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hormone structural gene.";
Nucleic Acids Ros. 7:305-320(1979)
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MEDILINE-83182010: Pubmed=7169009;
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-80034477; PubMed-386281;
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Homo sapiens (Numan).
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SEQUENCE FROM N.A.
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Hu R. M., Han Z. G., Sond H.-D., Pena Y.-D., Huang O.-H., Run S. N., Gu Y.-J., Huang C.-H., Li Y.-F., Jiang C.-T., Fu G., Zhang O.-B., Gu H.-J., Huang C.-H., Li Y.-F., Jiang G.-T., Fu G., Zhang O.-B., Xu S.-H., Gu J., Shi J.-X., Jin W.-F., Shang G.-Y., Wu T.-Y., Jin W.-F., Zhang G.-Y., Wu T.-Y., Ghen Z.-T., Chen M.-J., Chen J.-T., Jin W.-F., Zhang G.-Y., Wu T.-Y., Ghen J.-L., Gen J.-L., Jin W.-F., Zhang G.-Y., Wu T.-Y., Jin W.-F., Zhang G.-Y., Jin W.-F., Zhang G.-Y., Jin W.-F., Zhang G.-Y., Jin W.-F., Zhang G.-Y., Wu T.-Y., Jin W.-F., Zhang G.-Y., Jin W.-F., Zhang G.-Y., Jin W.-F., Zhang G.-Y., Jin W.-F., Zhang G.-Y., Wu T.-Y., Jin W.-F., Zhang G.-Y., Wu T.-Y., Jin W.-Y., J
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(In) Sriffiths K. (eds.):
Prolectin and carcinogenesis, Proc. fourth tecovus workshop prolection.
pp.13-20, Alpha Omega Alpha Press, Cardiff (1972).
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MEDLINE-71153968: PubMed-5279528;
Niall B.D., Hogen M.L., Sauer R., Kosenbium I.Y., Greenwood F.C.:
"Sequences of pituitary and placental lactogenic and growth horrouss:
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Proc. Natl. Acad. Sci. U.S.A. 68:866-869(1971).
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Li C.H., Dixon J.S., Liu W.-K.;
"Human pituitary growth hornone. XIX. The primary structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chapman G.E., Roders K.M., Brittain T., Bradshaw E.A., Pates C.J.,
Turner C., Cary P.D., Crane-Robinson C.:
The 26/000 Exceediat weight variant of human growth barmone.
Preparation and some physical and chemical proper'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE-22143935; PubMed-5144027;
Li C.H., Dixon J.S.;
"Human pituitary growth hormone, 32. The primary structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-710922028; PubMed-467545;
Bewley I.A., Dixon J.S., Li C.H.;
"Sequence comparison of human pituitary growth hormone, human
chorionic somatomamotropin, and ovine pituitary growth and
lactogenic hormones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Revised primary structure for human growth hotmone.";
Nature New Biol. 230:96-91( 971).
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                SEQUENCE FROM N.A. (ISOFORM 4).
IISSUE-Pituitary.
MEDLINE*20402571; Pobmed*10331946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-81117361: PubMed=7462247:
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MEDLINE-80130196; Pubmed=7356479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-71139765; PubMed-5279046;
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                                                                                                                                                                                                                                                                                                                                                                    Gene 39:247-254(1985).
                                                                                                                                                                                                                                                                                                                                                                                    [9]
SEQUENCE OF 27-217.
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Niall H.D.:
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X-FAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE~95075462; PubMed-7984244:
Somers W., UILSCH M., de Vos A.M., Kossiakoff A.A.;
Somers W., Citsch M., de Vos A.M., Kossiakoff A.A.;
The X-ray structure of a growth hormone-prolactin receptor complex.";
Nature 372:478-481(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- FUNCTION: Plays an important role in growth control. Its major role in stimulate to stimulate the liver and other ilsuses to screte IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cargili M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra D., Friedland L., Rolie A., Warrington J., Lipshutz R., Daiey G.Q.,
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                                                                                                                                                                                                                                                   MEDLINE-R2052997: PubMed-7028740;
Lovis T.J., Slogh R.N., Bonewald L.F., Seavey B.K.;
"Altered proteolytic cleavage of human growth hormone as a result of
demnidation.":
Lewis U.S., Borowald L.F., Lewis L.J., The 20, 700-dallon of the arise acid deletions. Income: Iceation of the uping acid deletions. "Prochem. Biophys. Res. Comman. 92:511-516(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystal structure of an antagonist mutant of human growth hormone, 5120R, in complex with its receptor at 2.9-A resolution.": 3.8iol. Chem. 271:32197-32203(1996).
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MEDLINE-97113023; PubMod-8943276;
Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLLINE-92196577; PUDMEDLLOGRAPHY (6.6)
Ge Vos A.M., Ultsch M.K-Osslakoff A.A.;
"Human growth hormone and extrace]lular domain of its receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $5-$TRUCTURE MODELING.
MEDLINE-881-90073: Pubmed-3447173;
Cohon F.E., Kuntz. T.D.; T.D.; "Prediction of human growth
"Prediction of the three-dimensional structure of human growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raumann G.;
"Growth hormone heterogeneity in human pituitary and plasma.";
Horn. Res. 51 Suppl. 1;2-6(1999).
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Chantalat L., Chirgadze N.Y., Jones N., Korber F., Navaza J.
Paylovsk A.G., Wlodawer A.;
The crystal-structure of wild-type growth-hormone at 2.5-A
resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                       Biol, Chem. 256:11645:11650(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crystal structure of the complex.":
Science 255:306-312(1992).
                                                                                                                                                                                                                DEAMIDATION OF GLN-163 AND ASN-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99321812: PubMed-16393484;
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61-0CT-1994 (Rel. 30, Last. sequence update)
828-FEB-2063 (Rel. 41, Last annotation update)
Somatotropin precursor (Grewth Hormone) (GH) (GH-N) (Fitutiary growth
                                           Sars
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                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Matazoa: Chordată, Craciala: Vertebrată: Eutel-eistumi:
Mammalia: Euteria: Primates: Catarrhizi; Corceptifiecidae:
Cerceptifiecidae: Macaca.
NCBI_TAXID=9544;
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                                                                                                      DB 1; Length 217;
                                                                                2 FPTIPLSRLFONAMLRAHRIHGIAFDTYQHFEERYIPKEOKYSPLQNP
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BY SIMILARITY.
BY SIMILARITY.
E -> 0 (IN REF. 2).
N > D (IN REF. 2).
Score 255; DB 1; Pred. No. 6.6e 25;
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 Mismatches

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PROSITE; PS00266: SOMATCIRO:IN_1: 1.
PROSITE: PS0038: SOMATCIRO:IN_2: 1.
Hormone: Pituitary: Signal.
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                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque).
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                                           Conservative
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HSSP: P01241; 1AXI.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Scmatotropin precursor (Growt: hormone) (GH) (GH-N) (Pituitary growth
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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SUSCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                         2 FPTIPLSRIFONAMIRAHRIHQIAFDTYQEFERAYIPKEGKYSFLQNP 49
                                                                           13 FPTIPLSRI, FDNAMSKAHRIHQLAFDIYQEFEBAYIPKEQKYSFLQNP 74
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Pred, No. 6.6e-25;
 Pred. No. 6.6e-25;
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28-FEB-2003 (Rel. 41, Last sequence update)
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                     M:smatches
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faterpro; IPR061400; Somatotropia.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EME, outstation the European Bloinformatics Institute. There are no restrictions on is use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Soc http://www.isb-sib.ch/announce/or send an email to license!sgo-sib.ch)
                                                                                                                           Wallis O.C., Wallis M.;

"Cloning and characterisation of a putative growth hormone escuding gone from the marmoset (Calithrix jacotos) of growth hormone sound marmoset (Calithrix jacotos) databases.

Submitted (AUG-2000) to the EMBL/GEBBBBAR/TUSH databases.

FUNCTION: Plays an important role in growth control. Its major role in stimulation of stimulation of secrete IGP-1. It stimulates both the differentiation and proliferation of myothesis it also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu J.C., Makova K.D., Adkirs R.M., Gibson S., J. W.H., "Episodic evolution of growth hormone in primates and emergence of the species specificity of human growth hormone receptor."; Mol. Biol. Evol. 18:945-953(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saimiri boliviensis boliviersis (Bolivian squirre, nonkey).
Eukaryota, Metazoa, Chordatz, Craniata, Vertebrata, Buteleostomi:
Mammalia, Butheria, Primates, Platyrrhini; Gebidae, Gebinae, Simmiri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gatis
                                                    Eukaryota, Motazoa, Chordata, Cradiata, Veriebrata, Eutheleusiomi,
Mammalia, Eutheria, Primates, Platyrrhidi, Calitrichidae,
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                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FPTIPLSRIPDNAMIRAHELHQLAFDIYQEFERAYIPKEQKYSFIQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPTIPLSKLLDNAMJRAHEJHOLIH FOLHT, TITTE THE FORTPESKYSKLONP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 249; DB 1; Length 217; 97.9%; Pred. No. 3.76-24;
1ve 0; Mismatches 1; lodels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E102151A12CE6192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Somatotropin precursor (Greath hormone).
28-FEB-2003 (Rel. 41, Last annotation applace)
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SOMATOTROPIN.
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BY SIMILARITY.
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             Somatotropin precursor (Growth hormone)
                                      Callithrix jacchus (Common marmoset).
                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAR: PEO0103: hormone: 1.
PROSITE: PS00266; SOMATOTRCPIN_1; 1.
PROSITE: PS06338; SOMATOTRCPIN_2; 1.
                                                                                                                                                                                                                                               tissues (By similarity).
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21265430: PubMed=11371582:
                                                                                                                                                                                                                                                                                                                                                                                                                      41; 1A22.
IPRC0140C; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: AJ297563; CAC03481.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hormone; Pituitary; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA;
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Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-394.32;
                                                                                        NCBI_TaxID-9483;
                                                                                                                                                                                                                                                                                                                                                                                                                       P01241;
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P58343:
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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FEEFFES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete 169-1. It stimulates both the differentiation and proliferation of myobjasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
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-:-FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGP-1. It stimulates both the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-2003 (Rel. 41, Created)
25-FB-B-2003 (Rel. 41, Last sequence update)
26-FB-2003 (Rel. 41, Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primatos, Cutarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid uptake and protein synthesis in muscle and other
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C
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-:- TISSUE SPECIFICITY: Expressed in the placenta.
-:- SIMILARITY: BELCAGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                          Africa acid upcum.
tissues (By Similarity).
SUBSUES (By Similarity).
SUBSUES (By Similarity).
SUBSUES SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Revol A., Esquivel D., Santiago D., Barrera-Saidana H.; "Independent duplication of the growth hormone gene in three Anthropoidean lineages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217;
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9515289992C529F7 CRC64:
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Pred. No. 3.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0336; SOMATOTROPIN.
PROSITE; PSOC266; SOMATOTROPIN_1; 1.
PROSITE; PSOC338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: AP339066; AAK62287.1; -
InterPro; IPR001400; Somatotropin:
Pfam: PF60103; hormone; 1.
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97.9&;
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79 1
208 2
217 AA;
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modified and this statement is not removed. Usage by and for connected, entitles requires a license agreement (See http://www.lsb-sib.ch/aphonnoe/or send an omail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MFDLINE-89307277; PubMed-2744760; Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Galinas R.E., Seeburg P.H., Galinas R.E., Seeburg P.H., evolution.*,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISSENRAS 1 AND 2).
MEDLINE-88243769; PubMed-3779057;
COOKE N.E., Ray J., Emery J.G., Lichaber S.A.;
Two distanct species of human growth agrammar-yarlang mRNA in the human placenta predict the expression of novel growth homone
                                                                                                                                                                                                                                                                                                                                                                                                                        P01242: P09587;
21-JUS-1986 (Rel. Gl. Created)
88-FEB-2603 (Rel. 41. Last sequence update)
15-SEP-2003 (Rel. 42. Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Humau).
Bukaryota, Metazoa, Chordatu: Cranlata, Vertebiata, Buteleostomi.
Mammaila: Butheria, Primates, Catarthini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The human growth bormone gone family: nucleotide sequences show recent divergence and predict a new polypeptide hormone.":
DNA 1:239-249(1982).
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                                                                                                                                                                                                                                                                                                      2 PPTIPLISALFUNAMILRAHRIHQIAFUTYQEFSENYIPKEÇKYSFLÖNP 49
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Igout A., Scippo M.L., Frankenne F., Hernen G.;
"Cioning and nucleotides equence of placental heH-V cDNA.";
Arch. Int. Physicial. Biochim. 96:63-67(1998).
                                                                                                                                                                                                                                           DB 1: Length 217:
1.6e-22;
thes I; Indels
                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=22388257; PubMcd=12477932;
Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.
                                                                                                                                                                                BY SIMILARITY.

BY SIMILARITY.

1592A429075677DE CRC64:
                                                                      DIGETRO: IPR001400; Scratchtropin.
Pfam: PFC0103; hormone: 1.
PROSITE; PS00266; SCMATCTROPIN.1; 1.
PROSITE; PS00206; SCMATCTROPIN.2; 1.
PROSITE; PS00389; SCMATCTROPIN.2; 1.
26 BY SIMLAKIT.
27 217 GROWIH HORRONE VARIANT.
                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                            90.8%: score 236:
                                                                                                                                                                                                                                                           Fred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISCEORM 1).
MEDLINE-83182010; PubMed-7169009;
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                                                                                                                                                      26 BN
217 GI
191 BN
215 BN
24990 NW
                                                                                                                                                                                                                                                         33.88;
                                                           EMBL; AF374233; AAL72285.1
                                                                                                                                                                                                                                    90.org Match
Best Local Similarity 33.88
Matches 45, Conservative
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                                                                                                                                                                 27 2
79 1
208 2
217 AA;
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SOM2_HUMAN
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Kiavsner R.D., Collius F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altechul S.F. Zeeberg B. Bretow K.E., Schaefer C.F. Bhat N.K., Hopkins R.E., Jordan E., Moor S.I., Wang J., Hisleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G M., Hong L., Biatchenko L., Marusina K., Farmer A.A., Rubin G M., Hong L., A Stapleton M., Scares M.B., Bonaldo M.F., Casavant I.L., Scheetz T.E., Rehestel M.J., Jsdin T.R., Toshlyuki S., Carninci P., Prange C., A Raha S.S., Loqueilaron N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Mczley K.J., McFernan K.J., Malek J.A., Gunsartne P.H., Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Madan A., Wodriques S., Sanchez A., Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C., Shercherled A. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Greer than 15,000 full-length haman and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCNIT: Nonomer, dimor, trimer, tetramer and pentamer, disulfide-
linked or non-covalently associated, in homopolymeric and
heteropolymeric combinations. Can also form a complex either with
GHBP or with the alpha2-macroglobulin complex.
SUBCELUMAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Glycoprotein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1sold=P01242-2; Sequence=VSP_006203;
Vote=No experimental confirmation available;
Vote=No experimental confirmation available;
-: TISSUE SPECIFICITY: Expressed in the placenta;
-: SIMIMARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event-Alternative splicing, Named isoforms=2, Name+1, Synonyms-GH-V1: IsoId=P01242-i; Sequence-Displayed; Name=2, Synonyms-GH-V2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGEN PEOCIO3; hormone: 1.
PROSITE; PSO0266; SOMATOTROPIN_1; 1.
PROSITE; PSO0338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 139240; -.
GO; GO:0005180; F:peptide hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CaterPro; IPR501400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99321812: PubMed-10393484:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:4262; GH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A28072; SIHUV2.
PIR; D32435; SIHUV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Placenta;
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SIGNAL
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PLL_HUMAN
P01243;
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                                                               N-LINKED (SLCNAC, . .) (POTENTIAL).
RLEDGSPRIGGIENGSYSKEDTKSHNDDALLKNYGLLYCFE
KDNDKVETELRIVQPRSVEGSOGF -> VRVARSITNDSAP
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PGGEGGKWNNERGRECOFSAWFILLFYHFABAGRWOPPFWA
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007370: 028494;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
Eukaryota, Merazoa, Chordata, Craniala, Vertebrata, Butelcostemi.
Mammalia, Eurheria, Primates, Catarrinni, Cercopithecidae:
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues.
SUBCELLIAR LOCATION: Secreted (My similarity).
IISSUE SPECIFICITY: Expressed in the placenta.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 FPTIPLSKLFDNAMLRARRLYQLAYDTYGEFEBAYILKBGKYSFLGNP 74
                                                                                                                                                                                                                                                                                                                                   Score 228: DF I: Leagth 217;
Pred, No. 1.66-21;
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                                                                                                                                                                         FIGSVLQOV (is isoform 2),
FFIId+VSP, 00623,
R -> W (IN dbSNP:8789),
FFIId+VAR, 0.4592,
I -> T (IN REF. 2),
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GROWTH HORMONE VARIANT
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91.7%;
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EMBL; L16555; AAA20180.1; -.
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Matches 44, Conservative
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DISULFID
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                                                                 CARBOHYD
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CHAIN
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SOM2_MACMU
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PIR; I67411; I67411

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MEDLINE-85036426; PubMed=6208192;
Selby M.J., Barta A., Baxter J.D., Bell G.I., Eberhardt N.i..;
Malysis of a major human chorionic somatomammotropin gene. Evidence tor two functional promoter elements.";
J. Biol. Chem. 259:13131-13138(1984).
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13-APR-1988 (Rel. 07, Last sequence update)
15-SFP-2003 (Rel. 42, Last annotation update)
Lactogen precursor (Chorlomammotropin) (Chorlonic somatomammotropin).
CSH: AND CSH2.
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Barrera-Saldana H.A., Sceburg P.H., Saunders G.F.,
Two structurally different genes produce the same secreted human placental lactogen hormone.";
J. Biol. Chem. 258:3787-3793(1983).
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Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SNA 6:59-70(1987).
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MEDILINE-87161235; PubMcd-3030680;
Hirt H., Kinellman J., Birnbaum M.J., Chen E.Y., Seeburg P.H.,
Eberhardt N.L., Barra A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%; Score 199; DB 1; Length 217; 77:1%; Pred. No. 7e-18;
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HSSP, P01241; 1860.
InterPro: IPR031460; Somatotropin.
Ptam: PF05103; Normoney, 1.
PKINTS; PR00636; SCMATOTROPIN.
PROSTTE; PS00266; SCMATOTROPIN.1: IPROSTTE; PS00338; SOMATOTROPIN.2: 1.
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Genomics 4:479-497(1989)
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Seeburg P.H.;
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J00118; AAA98621.1;
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MEDLINE-7917308:: Pubmed-438159;
Schneider A.B., Kowalski K., Russell J., Sherwood L.M.:
*Identification of the interchain dishiride bonds of dimeric human placental lactogen.;
5. Biol. chem. 254:3782-7737(1979).
-: FUNCTION: SHRILAR TO THAT OF SONATOTROPIN.
-: FUNCTION: SHRILAR TO THAT OF SONATOTROPIN.
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO THE SONATOTROPIN/PROLACTIN FAMILY.
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Li C.E., Dixon J.S., Chung D.J.
Amino acid sequence of buran chorionic scratoscarbotropic.";
Arch. Ricohem. Biophys. 155:95 ULC(1973).
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Sherwood L.M., Handwerger S., McLaurin W.D., Launer M.:
"Amino-acid sequence of buran placental lactogen.";
Nature New Biol. 233:59-61(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M.;
Nature New Biol. 235:64-64(1972).
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UNA 1:239-249(1982).
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Lirzer D.I.H., Talamantcs F.;
"Nucleotide sequence of mouse prolactin and growth hormone mRNAs and
expression of these mRNAs during pregnancy.";
J. Biol. Chem. 260:9574-9579(1985).
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Das P., Meyer L., Seyfert H.-M., Brockmann G., Schwerin M.;
"Structure of the growth hormone-encoding gene and its promoter in
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Mammalia: Eutheria: Rodentia, Sciurognathi; Muridae; Musinae; Mus
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01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          PROSITE: PSGU266; SCHATOTROPIN_1; 1.
PROSITE: PSG0338; SCHATOTROPIN_2; 1.
Hormone; Placenta; Multigene family; Signal.
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Gil CR GH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LACTOGEN.
                                                                                                                                                                                                                                       EMBL: BC002717; AAE02717.1; --
EMBL: BC002921; AAH0521.1; --
EMBL: BC0020756; AAH20756.1; --
FIR; A26449; A2649.
FIR; C32435; LCECC.
GENEW: HGNC:2446; CSH1.
GENEW: HGNC:2441; CSH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25020 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00103; hormone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2:3
191
215
208
215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
154
217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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Somatotropin (Growth hormone).
                                                                                                              Onery Match
Hust Local Similarity
Trowns 32: Conserva
                                                                                                  190 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obery Match
Best Local Similarity
Matches 32, Conserv
 HSSP; P01241; 1AXI.
                                                                         52
190
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P10755;
                                                                                                                                                                                                                                                                    SCMA_LOXAF
                                                                         DISCLETO
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
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                                                                                                    SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                              P20392;
                                                                                                                                                                                                                                                        SOME LOXAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMA_VULVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                          RESULT 12
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                                             This SWISS-TROT entry is copyright. It is prediced through a collaboration between the Swiss institute of Buoinformatics and the FMBL situation the European Bioinformatics Institute. There are no residences on its use by soon-profit institutions as long as its entern is to no way entities required and this statement is not retroyed. Tagge by and in commercial entities required a license agreement (See http://www.isb-sib-ch/agreeneet
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Csipova T.A. Bulatov A.A. Pankov Y.A.;

Strangments of sei whale (Balaincoptera borealis) somatorropin.":

Bioorg. Khim. 4:1589-1599(1978)

-1-FUKCTION: Plays an important role in growth control. I.s major role in stimulating body growth is a stimulating to secrete igfort. It stimulatios both the other tissues to secrete igfor. It stimulatios both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in miscle and other
                                                                                                                                                                                                                                                                                                                                                                                              Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balaenoptera borealis (Sei whale).
Bukaryota: Metazoa: Chordata: Craniata: Vertobrata: Euteleostori:
Mammalia: Butheria: Cetartiodactyla: Cetacca: Mystinett;
Balaenopteridae: Balaenoptera.
NCBI_TAXID=9768:
amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE SCHATOTROPIN/FRELACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     DB 1: Length 216;
                                    SIMINARITE: BELONGS TO THE SOMATOTECPIN/FECLACIEN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                    2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEGKYSFLON 48
                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILABITY.
SOMATOTROPIN.
BY SIMILABITY.
BY SIMILABITY.
BY SIMILABITY.
BY 98666A3AE25D65FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yudaev N.A., Pankov Y.A., Bulatov A.A., Osipova I.A.;
"Amino acid sequence of seiwhale somanotropin.";
Biokhimiia 47:1659-1669(1982).
                                                                                                                                                                                                                                                                                                                                                 62.1%, Score 151.5; DB 1; Fred, NO. 3.5e-13; Pred, No. 3.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61-007-1993 (Rel. 27, Created)
01-007-1993 (Rel. 27, Last Sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                    PIR, B23911; STMS.
HSSP, P01246; 15ST.
MOD. MC1246; 15ST.
InterFig. 1PR001400; Somatotropin.
Fram: PF00103; hormone; 1.
PRCSITE: PS00366; SOMATOTROPIN.; PRCSITE; PS00388; SOMATOTROPIN.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
              tissnes.
SUBCELLULAR LOCATION: Secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somatotropin (Growth hormore)
                                                                                                                                                                                                                                                                                                                                         24716 NW;
                                                                                                                                                             EMBL; X02891; CAA26650.1; ...
EMBL; Z45653; CAA86658.1; ...
                                                                                                                                                                                                                                                                              Hormone, Pituitary, Signal
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 58.1
nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                      216
189
                                                                                                                                                                                                                                                                                                      27 2
78 1
206 2
216 AA;
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P33092;
                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOMA_BALBC
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6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loxodonta africana (African elephant).
Sukaryota Metazoa, Chordata, Craniata: Vertebrata, Euteleostomi;
Mammalia: Eutheria; Proboscidea; Elephantidae: Loxodonta.
NCHI_TaxID=9785;
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                                                                                                                                                           DB 1: Length 190;
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80
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                                                                                                                                                                                                                            2 PPTIPLSRIFFNAMLRAHRLHQLAFDTYOEFEEAYIPKEQKYSFLON
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                                                                                     BY SIMILARITY.
BY SIMILARITY.
09FBFF6DB14A75D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 188 BY SIMILARITY.
190 AA; 21761 MW: 054860813DH741F2 CRC64;
                                                                                                                                                     61.7%; Score 160.5; DB 1968.1%; Pred. No. 4.1e-13;
Live 6; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.3%; Score 159.5; DB I
llarity 68.1%; Pred. No. 5.5e-13;
Conservative 6; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C1-30L-1989 (Rel. II, Created)
OI-JUL-1985 (Rel. II, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
Electric IPR001400; Sometotropin, Pfan, PF01013; Normanne; PF05; Electric PS00266; SCMATCTROPIN_: 1 PROSTUE; PS00318; SCMATCTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                        21835 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatotropin (Growth hormone).
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                   STANDARD
                                                          PRODUCE, ....
Hormone, Pituitary.
52 163
                                                                                                      188
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Cell. Endocrinol. 150:121-128(1999).
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es 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                  tissues.
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      Decived 1.S., Teske E., van Garderen E., Rutteman G.R., Mol J.A.; "Extrapituitary growth hormone expression in the dog is initiated at the normal pituitary transcription start site in the mammary gland and at multiple upstream sites in lymphoid cells."; Submitted (MAR-1997) to the EMBL/GenBank/DDSJ databases.
                                                                                                                                                                                                                                                            Lantinga-van Leeuwen I.S., Oudshoorn M., Mo. J.A.;
"Canine mammary growth hormone gene transcription initiates at the
pituitary-specific start site in the absence of P:t-1.";
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Ascacio-Martinez J.A., Barrera-Saldana H.A.;
"A dog growth hormone cDNA codes for a mature protein identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Bukaryota: Metazoa; Chordata: Craniata; Verfebrata; Enteleostori:
Mammalia: Butheria: Carnivora: Fissipedia: Canidae; Canis.
                                                    Eukaryota: Metazoa; Chordata; Craniata: Vertebrata: Buteleostomi;
Mammalia: Butheria: Carnivora; Fissipodia: Canidae; Vulpus.
NCBL_Taxib=9627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE SOMATOTROPIN/FROLACTIN FAMILY.
HSSP: P01246: 1887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FB 1; Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PPTIPLSRLFDNAMLRAHRUHQLAFUTYQBFEFAYIFKEGKYSFLQN 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14F37H9C1CBB802C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%: Score 159.5; BB 1
68.1%: Pred. No. 5.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p3371; Ogrqfs;
01-FEB-1994 (Rel. 25, Created)
16-CCT-2001 (Rel. 42, Last sequence update)
Somatotropin precursor (Growth hormone);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03153; hormone: 1.
PROSITE; PS03266; SOMATCHROPIN_1; 1.
PROSITE: PS00338; SOMATOTEOPTN_2; 1.
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MEDLINE-99337113; PubMed-10411306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPROG1400; Somatotropin.
                                                                                                                                                                                                        TISSUE-Pituitary;
MEDLINE-89254275; PubMed-2722401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 163 B
180 189 B
190 AA: 21731 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                              Vulpes vulpes (Red fox).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 143:277-280(1994).
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Best Local Similarity
Matches 32; Couserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pig growth hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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-i- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete [GF-1. It stimulates both the differentiation and proliferation of myobiasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castro-Peralta F., Barrera-Saldana H.A.; "Cloning and sequencing of cDNA encoding the cat growth hormone."; Gene 160:311-312(1995).
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Eukaryota; Metazoa: Chordata; Craniata; Vertobrata; Euteleostomi;
Marmalia; Eutheria; Carnivora; Fissipedia; Felidae; Pelis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE SCMATOTROPIN/PRCLACTIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
SCMATOFROPIN.
BY SIMILARITY.
BY SIMILARITY.
S -> G (IN REF. 1).
N -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%: Score 159.5; DB 1
68.1%: Pred. No. 6.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.3c
6, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P01246; 1831.
InterPro: IPR01400; Somatotropin.
Pidm; P60103; hormone; 1.
PRINTS: PR00836; SOMAIOTROPIN.
PROSITE; P500256; SOMAIOTROPIN.1; 1.
PROSITE; P500338; SOMAIOTROPIN.2; 1.
                                                                                                                                                                                                    Secreted
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MEDLINE*95369713; PubMed*7642118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pituitary;
MEDLINE-96194906; PubMed-8654953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 AA; 24468 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: 723067; CAA80601.1; -...
EMBL: 092533; AAF21502.1; -...
EMBL: AF069071; AAD43366.1; -...
PIR: 146145; 146145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone, Pituitary: Signal
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This SWISS-PROT entry is copyright. It is produced through a cultabase-then between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions in its use by non-profit institutions as inong as its content is in to why modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.tsb-sib.ch/anneurory or send an email to license@lsb-sib.ch).
FUNCTION: Plays an important tole is growth routed. Its major role in stimulating body growth is to slimmiate the liver and other tissues to screeke 10F-1. It stimulates both the stimulation and proliferation of myoplasts. It also stimulates amino acid uptake and proliferation of myoplasts. It also stimulates amino acid uptake and proliferation of myoplasts. It also stimulates tissues.

SUBJURIAN LOCALION: Serveted.

SUBJURIAN PRINTY: BRIDNES TO THE SOMMYOTEOFIN/PROLATIN FAMILY.
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tive 6; Mismatches 8; Indels 1;
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BY SIMILARITY
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N -> T (1N REF. 2).
T -> A (1N REF. 2).
C -> A (1N REF. 2).
C -> P (1N REF. 2).
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EMBL, U13390; AAA96142.1; ...
PIR, JC4632, JC4632, JC4632, JC4632, JC4632, JC4632, JC4632, JC4631, JC4632, JC4631, JC463
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Best Local Similarity 68.1:
Matches 32; Conservative
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216 AA;
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DISULFID
CONFLICT
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Search completed: September 15, 2003, 12:01:29 Job time : 5.56631 secs 091021 capra hiro:
091021 capra hiro:
091049 bos indicus
068875 callithrix
028957 sus scrofa
09060 traqulus ja
091059 macropus ru

09jkg0 cavia porce

095MT6 095MT6 09TU21 09T0W9 08M175 028957

09BEB9 09TRI9 09PU72 091386

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09912 cynops pyrr 099136 amia calva 09540 canis famil 014406 homo sapien 08988 anser anser 019534 ovis aries 046474 felts silve P78451 homo sapien 030471 heterophens 080710 heterophens 080710 heterophens 080710 heterophens 080710 clarias gar 09075 clarias gar 09076 clarias gar 09076 clarias gar 09076 clarias gar 09076 clarias gar 09077 clarias gar 09078 clarias gar 09078 clarias gar 09078 clarias gar 09078 carassius a

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OBQFN2

OM protein -

Run on:

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Growth hormone.
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Q07367 macaca mula
Q07369 macaca mula
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Q8mq9 steles geof
Q8m74 callithrix
Q70615 spalax leuc
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Copyright (c) 1993 - 2063 Compagen Itd.
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Match Length DB
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Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Atelinae, Ateles.
NCF1_TaxiD+9509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                            Revol A. Esquivel D., Santiago D., Barrera-Saldana H.:
Revol A., Esquivel D., Santiago D., Barrera-Saldana H.:
Independent duplication of the growth hormone gene in three
Anthropoldana lineages.",
Submitted (ARR-2001) to the Embi,/GenBank/DDBJ databases.
Embi, AP374234, AAL7286-1;
Interpro, TPR061040, Schatotropin.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00266; SOMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24894 MW; 425829FF41EEAAR6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 95.8%; Score 249; DB 6; Length 21 Best Local Similarity 97.9%; Pred. No. 1.2e-25; Matches 47; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  Atcles geoffroyi (Black-handed spider monkey).
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AL LGNMENTS
                                                                                                                 PRT;
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61-MAR-2002 (TrEMBLRel. 20,
01-MAR-2003 (TrEMBLRel. 23,
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Best Local Similarity
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TISSUE-Placenta;
MEDINE-94088724: PubMed-8404617;
MEDINE-94088724: PubMed-8404617;
MEDINE-94088724: PubMed-8404617;
Cloning of sour growth hormone/Ahorion's somesommemoriopialities
complementary decayts monkey placenta.";
pregrancy in the thesus monkey placenta.";
pregrancy in the thesus monkey placenta.";
EMBL: 01555; AAA18840.1:
HSSP: PO15141: JAX.1
FREPPO: TREG-1403; hormone: InterPO: Pram. PFO0003; hormone: InterPO: PFO0
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MEDLINE-888373737; PubMed 9729637;
Boguszewski C.L., Svenskon P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carisson B.;
"Closing of two nove; growth hormone transcripts expressed in lumin
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Mammalia, Eutheria, Primates, Catarrhidi, Corcopithecidae,
Cercopithechae, Macaca,
NCRLTAXID=9544;
                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazda; Chordana: Craniata; Vertebrata; Eutheleost mis
Mammalia; Eutheria: Primates: Catarthini; Beninidae; Here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
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tive 9; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 PPTIPLSREFONAMERAFREYGLAYDIYQEPSHAYILKROKYSFLÖNP
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01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Somatotropin 2 precursor (Growth hormone 2) (Fragment)
Magaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 212 AA; 24525 MW; 275091106256E6FF GROS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14CC7F8CP75D91C8 CRC64;
01-JAN-1958 (TERRITEL. 35, Created)
01-JAN-1998 (TERRILEL. 35, Last sequence update)
01-DBC-2601 (TERRILEL. 19, Last annotation update)
Placental growth hormone isoform EdH-V4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AFOGOGIACL Metab. 83:2878-2485(1958).
EMBL: AFOGOGO: AA871829.1: -.
HSSP: P01241: 1A22.
InterPro: IPROJ1400: Somatotropia.
PROSTE; PSO0266; SCMATOTROPIA.:
PROSTE; PSO0266; SCMATOTROPIA.: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AM.
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27101 NW:
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Best Local Similarity 78.73
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 91.7*
Matches 44, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 AA:
                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9606;
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01-NOV-1996
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QC7368
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MEDLINE-94009724: PubMed-8404617;
MEDLINE-94009724: PubMed-8404617;
Goles T.G., Darning M., Pisher J.M., Fowler P.D.;
Endocring of four growth Permone-formation of Scattering of four growth Permone-formation of Fowler growth Goles Gol
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01-NOV-1996 (TEMBLE). 01, Last sequence update)
01-MAR-2003 (TEMBLE). 03, Last annotation update)
chorionic somatomanmotropin-3.
chorionic somatomanmotropin-3.
Eukaryota, Metazoa, Corodata, Craniata, Vertebrara, Eulelcostomi;
Mammalla, Eutheria, Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Madada mulatta (Rhesus mādaque).
Enkarydota Merkazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Bulheria; Primades; Catarrhini; Cercopithecidae;
Cercopiticocimae; Madada.
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Pfam: PF0C103; hormone; I.
PRINTS; PR00836; SCMATOTROPIN.
SEQUENCE 217 AA; 24942 MW; FFSAA8915131F2BC CRC64;
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SEQUENCE 217 AA: 24874 MW; FIEB6AFDBBA18185 CRC64;
007367
007367,
0-1007.1996 (TrEMELREL 0), Created)
0-1007.1996 (TrEMELREL 0), Last sequence update)
0.1007.2003 (TrEMELREL 23, Last annotation update)
0.1007.1003 (TrEMELREL 23, Last annotation update)
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Pred. No. 3.8c-19;
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78.7%; Pred. No. 9e-21;
Live 9; Mismatches
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Pfam; PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
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Best Local Similarity 78.7
Matches 37, Conservative
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Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Callithrix.
                     Arcles geoffroyi (Black-handed spider monkey).
Eskaryota, Metazoa, Chordata, Craniata, Vortebrata, Euteleostomi;
Mammalla, Eutheria, Primates, Platyrrhini, Cebidae, Atelinae, Ateles.
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Wallis O.C., Wallis M.;
"Characterisation of the GH gene cluster in a new-world monkey, the marmosterisation of the GH gene cluster in a new-world monkey, the marmoster (Calithrix jarchus).";
J. Mol. Endocrinol. 0:0-0(2002).";
EMBL; AJ409811; CAD34012.1;
InterProy. IPPSO1409; Somatotropin.
Prim: PPS0103; hormone 1: PRIMIS: PR00134; hormone 1: PRIMIS: PR00135; SOMATCIROPIN.
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                                                                                                                                                   Mevel A., Esquivel D., Santiago D., Rarrera-Saldana H.;
"Independent duplication of the growth hormone gene in three Authopoidean lineages.";
Submitted (APR-201) to the EMBL/GenBank/DDBJ databases.
EMBL, AF31235, AA172397.;
Interpro: PRR001400; Somatotropin.
Ptam: PP00103; normone; 1.
PRINTS: PR00836; SOMATOTROPIN...;
PROSTITE, PS00266; SOMATOTROPIN...;
PROSTITE, PS00318; SOMATOTROPIN...;
SEDUENCE 217 AA; 25293 MW; 741745A1B75C053E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 FPRIPLSRLFGDAMLRAHOLHQVAFDTYQELEENGIPKKQKYFFLRNP 74
                                                                                                                                                                                                                                                                                                                                                                                                                           Oucry Match 75.0%; Score 195; DB 6; Length 217; Best Local Similarity 77.1%; Pred. No. 2.5e-18; Matches 37; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
GROWTH HORMONE-LIKE PROTEIN 6.
5ECF148798278F1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 PRIPESREPROALRARQEHREALETYREFEKNCVPKEQKYFELRNP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPTIPLSRIPUNAMIRAHRIHQLAFOTYQEFEBAYIPKEQKYSFLONP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 65.4%; Score 170; DB 6; Length 21 Local Similarity 68.1%; Pred. No. 6.1e-15; es 32; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PTIPLSKLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP
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Last annotation update)
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01-001-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone-like protein 6 precursor.
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01-AUG-1998 (TrEMBLrel. 07, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Callithrix jacchus (Common marmoset)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS003.88: SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 PO
217 GR
25177 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 2
217 AA;
                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                          NCBI_TaxID-9509;
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Matches
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                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Croated)
01-NOV-1996 (TrEMBLrel. 01, iast sequence update)
01-NAR-2003 (TrEMBLrel, 23, Last amnotation update)
Chorionic somatomammetropii CS-2 (Chorionic somatomammetropii hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
    90.50
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MEDLINE-83337277; PubMed~2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Selinas R.E.
Seeburg P.H.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDGINE-91102558; PubMed-1980158;
Vnencak-Jones C.L., Phillips J.A. 171.;
Vnencak-Jones C.T., Phillips J.A. 171.;
Vnencak-Jones For growth hormone gene deletions in homologous regions outside of Alu repeats.
Science 250:1745-1748(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The homan growth hormone locus: nucleotide sequence, biclody, and evolution. \footnote{\mathbb{Z}}_2
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9605;
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  ċ
                                                                         3 PTIPLSREFINAMURAHRUNGGAFBTYGEFEBAY19KEOKYSFLØNP 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 TYPLSRLFDHAMLQAHRAHQLALDTYQEFEETYTEKDQKYSFLHD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausherg R.;
Submitted (JUL-2002) to LDE EMBL/SenBank/UDBJ databases.
EMBL; 303071; AAAS2553.1; ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg K.)
Submitted (JAN-2002) to the EMBL/GenBack/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24994 NW: 39PAACDDB6B2E951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                       217 AA
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  8; Mismatches
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PRINTS, PRO0836; SCMAIGTROFIN.
PROSITE: PSO0266; SCMAIGTROFIK_1; 1.
PROSITE: PSO0388; SCMAIGTROFIK_2; 1.
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                                                                                                                                                                                                       PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR031400: Somatciropin.
Pfam: PF00103: Normone: 1.
PRINTS: PR09836: SOMAIGTROFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: BC022644: AAH22044.1: -.
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01-MAR-2002 (TrEMbLrel, 20,
01-MAR-2002 (TrEMBLrel, 20,
01-0CT-2002 (TrEMBLrel, 22,
Growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0
Matches 36; Conservative
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35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 4:479-497(1989)
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA;
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TISSUE-Placenta:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.
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  Matches
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Q14407
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Guery Match
Best Local Similarity 68.18;
Matches 32; Conservative (
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PREL:MINARY:
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Best Local Similarity
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CHAIN 27 2
SEQUENCE 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCB1_TaxID+9728;
                                                                                                                                                                                                                                                                                                                 Delphinus.
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QBHYE5
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SOLUTION DE LA COMPANIO DEL COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO 
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                                                                                                                                                                                                                                                                             Lioupis A., Nevo E., Wallis M.: **Cloning and characterisation of the gene encoding noie ra' (spalax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDGINE-99560468: PubMed-19051323:
MEDGINE-99560468: PubMed-19051323:
Getano A.R., Pomp D., Marray J.D., Bowling A.T.,
"Comparative mapping of 18 equine type I genes assigned by schild hybrid analysis.";
cell hybrid analysis.";
Mamm. Genome 10:271-276(1993).
EMBL; AROY5899: AAD2559211;
InterPro; IPR001400; Somatotropin.
                          Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eureleostami;
Mammalia: Eutheria: Rodontia: Sciurodnathi: Arridae: Spalacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa: Chordata: Graniata: Vertobrata: Euteleostum::
Mammalia: Eutheria: Perissodactyla: Equidae: Equis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 FPAMPESNLFANAVLRAG-HEGLAADSTEKKEFERAYTFEGGRYS-1QN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPTIPESRLFDNAMLRAHRLHQLAFDTYOSFEEAYIPKEGKYSFLON 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 26 FOTENTIAL.
27 216 GROWTH HORNONE.
216 AA; 24627 MA; EEABBAS23BAOADFE CMC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.7%; Score 160.5; DB 11
Best Local Similarity 68.1%; Pred. No. 1.2e-13;
Matches 32; Conservative 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 159.5; 38 h
Pred, No. 3.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 AM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PROGRAGE SOMATOTROFIN.
PROSITE, PSOSS66: SOMATOTROPINEL: 1.
PROSITE, PSOSS6: SOMATOTROPINEL: 1.
                                                                                                                                                                                                                                                                                                                                           ehrenbergi) growth hormone.";
J. Mol. Endocrinol. 22:29-36(1959).
HEBE: AJOUSBIB: CARO6716.1;
HSSP: POLZ41: LAXI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro/ IPRC01400; Somatctropin.
Pfam: PF06103; Sormone: 1.
                                                                                                                                                                                                                                            MEDLINE-99124645; PubMed-9924177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00103; hormone; 1.
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Best Local Similarity 68.1
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Equus caballus (Horse).
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                      NCB1_Tax10-30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9796;
                                                                                                                            Nannospalax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9TV91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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Q8M173
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                                                                                                 Delphinus delphis (Saddleback dolphin) (Black sea dolphin).
Eskaryota, Metazos, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti; Delphinidae,
                                                                                                                                                                                                                                            TISSUE-Liver;
Manio: Z., Wallis O.C., Wallis M.;
"Cloning and characterisation of the GH gene from the common dolphin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth formone precursor.

Growth formone precursor.

Saluropoda melanoleuca (Giant panda).

Bukaryota: Metazoa; Chorduta: Craniata; Vertebrata; Buteleostomi;

Manemalia: Butheria; Carnivora: Fissipedia: Ursidae; Alluropoda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.3%; Score 159.5; DB 6; Length 216; 68.1%; Pred. No. 1.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TSOUTH TO THE PROPERTY SEQUENCIALITY: 2 Lang A.: "Cloning and expression of cDNA encoding growth hormone from Allitropoda melanoleuca": Submitted (AUG-2002) to the EMBI/GenBank/DDBJ databases. BMBL AF$40936: AAN77228.1; "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 159.5; DB 6; Length
Pred. No. 1.6e-13;
6: Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FPTIPLSRLFDNAMLRAHRLHOLAFDTYOEFEEAYIPKEQKYSFLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FPTIPLSRLFUNAMLRAHRUHQLAFDTYQEFEBAYIPKEQKYSFLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8: Indels
                                                                                                                                                                                                                                                                                                   216 GROWTH HORMONE.
24509 MW: 1EC467A84CCFEBC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. 44EC17EC44BCB056 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Created)
91-KAR-2003 (TrEMBLrel. 23, Last sequence update)
91-NAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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SEQUENCE 216 AA; 24383 MW;
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RESULT 13

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Job time : 22.1434 secs
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095MJ5;
   RESULT 15
                                     095MU5
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last senotation update)
Growth hormone precursor.
Growth hormone precursor.
Exala proceilus (Galnea pig).
Exkaryota, Metazoa: Chordata; Craniata: Vertebrata; Extelessional Manmalla: Furbaria: Rodencia: Hystricomethis: Gaviade: Caviade: Caviade
                                                                                                                                                                                                                                                                                Eukaryota; Melazoa; Chordara; Craniata; Vortebzata; Euteleostemi;
Mammalia; Eutheria; Rodentra; Schurognathi; Muridae; Murinae; Mus
NCBL_TaxiD=16090;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nguyen T.N.K., Liebhaber S.A.:
"Mouse Growth Hormone Locus: Nucleetide Sequence and Phylogenetic
Analyses:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë
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Sequence From N.A.
Odorico D.M., Fuller P.J., Scrington A.C.;
"Cloning and sequence of graines pig arowth hormone (GE).1:
"Cloning and sequence of graines by arowth hormone (GE).1:
"Submitted (FES-2000) to the EMBL/GenHank/DDHC databases.
BMBL: AP233853; AAP36409.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.8%; Score 155.5; UB 11; Length
66.0%; Pred, No. 5.5e 13;
tive 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PPTIPLSRLFDNAMERAHRLHQLAFDTYGEFERAYIPKEGKYS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FMBL, U3436.2.
HSSP: P01241: LAX1.
InterPro: InterPro: LAX1.
Pfam: PF06103: horrore: 1.
PRINTS: PR00R86: SCMATOTROPIN.
PROSTITE: P800R86: SCMATOTROPIN.
PROSTITE: P800R38: SCMATOTROPIN.
SEQUENCE 216 Aa; 24682 MW; F02AG6DA02*30H18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 26 POTENTIAL.
27 216 GROWTH HORMONE.
216 AA: 24822 MW: 45996BEL19808DD3 CRC64;
                                                                                                      01-MAY-2000 (TrEMBLrel. 13. Created)
01-MAY-2000 (TrEMBLrel. 13. Last sequence update).
01-MAR-2003 (TrEMBLrel. 23. Last ancotation update)
Growth hormome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.2%; Score 154; Db 11;
67.4%; Pred. No. 8.9e-13;
ative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 216 AA
                                     216 AA.
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Pfam; PF00103; bormone: 1.
PRINTS; PR00836; SOMATOTROFIN.
PROSITE; PS00266; SOMATOTROFIN.
PROSITE; PS00338; SOMATOTRCPIN.
1: 1.
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Best Local Similarity 66.03
Matches 31: Conservative
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                                     PRELLMINARY:
                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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Best Local Similarity
Matches 29, Conserv
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SIGNAL
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Q9R2C3
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                                     HODER REPRESENTATION OF THE PROPERTY OF THE PR
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1D GGENES
PRELIMINARY:

AC 0958125

DT 01-DEC-2001 (TrEMBLEC: 19, Created)

DT 01-DEC-2001 (TrEMBLEC: 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLEC: 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLEC: 13, Last annotation update)

OS Tarisus banconus (Mestern tarsier) (Horsfield's tarsier)

ON MCBLTAXTOG9477;

NN CBLTAXTOG9477;

NN CBL
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OM protein

Run on:

Total number

Database

20070000

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Searched:

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Mutant human 22kDa
Human growth hormo
Human growth hormo
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Sequence of protei
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Natural human 22kD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth Hormone, chaperone, intramolecular, insulin, precursor, folding, conformation, chimeric protein, cleavable, recombinan
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Human
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Human
Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
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                                                                                                                                                                                                                                                         ABGS4908
ABG94909
ABG94910
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ABC94912
ABC94913
ABC94914
ABC94915
ABC94916
ABC94916
ABC94919
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ABG94921
ABG94922
ABG94923
ABG94924
ABG94924
                                                        AVI 5809

AAYC4396

AAYO4327

AAO17485

AAO17486

ABG94865

ABG94866

ABG94866

ABG94864

ABG94864

ABG94864

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ABG94864
                AAP61033
AAP81226
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 oldsymbol{\pi}
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   WPI; 1999-610839/52
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 WC9950302-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JAN-2000
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\\ \dagger \da
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
AAY42856
Chimeric protein,
Human growth hormo-
Human growth hormo-
Human anti-angloge
Human nerve growth
Human growth
Fusion protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human growth Lormo
Human apti-angloge
                                                                                                  September 15, 2003, 11:44:15 : Search time 64.6:08 Soronds (without alignments) 225:942 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                              1 MFPTIPLSRLFDNAMLRAHR.......NLELLRISLLLISSWLERVQ
            GenCore version 5.1.f
Copyright (c) 1993 - 2003 Companen Ltd.
                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                         1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first is summaries
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AAW 92265
AAY 42861
AAP 91041
AAP 9129
AAP 91294
AAR 11740
                                                                        protein search, using sw model
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Gapop 16.0 , Gapext 0.5
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Length: 2600000000
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Match
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Maximum DB seq
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growth h

hormo

hormo

growth growth

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hormo hormo

growth

hormo

growth

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This sequence represents an N-terminal transmist of hosen growth borneus (hGH) which is a component of a chimeric protein (AAV42661) which also contains a functional precursor (AAV42869). The hGH portion of the chimeric protein acts as an intramplementary character (TMC) for the chimeric protein acts as an intramplementary of acts and the chimeric protein to be removed after (Diding has taken place). Inker while a C-terminal Arg residue (AAV42867) unables the hGH portion of the chimeric protein to be removed after (Diding has taken place). Production of recombinant haman insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a bigher yield of human insulin with correctly linked cysteine bridges with human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a microorganish host, but sequence the foliang of the fusion protein and decrease the intermolecular the fusion proteins thus allowing folding of the fusion proteins thus allowing folding of the fusion proteins, thus allowing folding of the fusion proteins, thus allowing folding of the fusion proteins, thus allowing folding of the fusion proteins and decrease the interminant steps of cyanogen bromide cleavage, exidently setting the profession and related purification steps and this here eliminated, along with the last of the content and the last of the last of the content and the last of the last of the content and the last of the last of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fluman, anti-angiogenic; prolactin; placental lactogen; LED; anglocenesis; growth hormone; hGH; hGH-V; capillary endothelial cell proliferation; placental vascularisation; pregnancy; treatment; andiogen; disease; tumour; thhibitor; malignant; angiofibrone; arreinovenous malformation; artificitis; atherosolerotic plaques; corneal arcit neovascularisation; wound healing; proliferative retinopathy; deciler decentation; trachment proliferation; quelitis; fracture; caler-weber synctome; psoriasis; libroplasia; scheroderic contacted; surcome; vascular addession; ulcor; leukalomia; reproductive disorder; contacted; returdation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEPTIPLSRIFUNAMIRAHRIHQLAFDTYQEFEEAYIPKEOKYSFLONFOTSLSFSSIF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 470; DB 20; Congth 92: 100.0%; Pred, No. 5.8e-40; Liviels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti-anglogenic peptide 16K hGH Met-1Prol33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IPSNREETOQKSNLELLRISLLLTOSWLEPVO 92
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100.0%; c.
                            Claim 5; Page 28: 46pp; English.
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Best Local Similarity
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properties can be used for preventing or treating e.g. maignant tumours, any filterand, arteriovencies malformation, arthritic such as rheumatoid artifits, atterosciencic plaques, conneal graft mechasitation.

Glayed wound healing, proliferation, granulations such as those occurring the technopathy, macular degeneration, granulations such as those occurring in hemophilic joints, imappropriate vascularisation in wound healing such as hyperticipits scars or keloid scars, neovascular glaucoma, ocular tumour, uveitis, non-union fractures, Oslar-Weber syndrome, psoriasis, pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours, Kaposi's sarcoma, trachoma, vascular adhesions, chronic varioose ulcers, loukaemia, and reproductive disorders such as follicular and luteal cysts and choriocarcinoma. They can also be used as contraceptive agents. DNA encoding the peptides can be used in gene therapy. The measurement of abnormal levels of N-terminal fragments of health, hGH-V, prolactin or hPL can be used in assays for impairment of vascular development associated with pre-eclampsia, intrauterine growth retardation, and placental
                                                                                                                                                                                                                                                this invention describes novel human anti-angiogenic peptides derived from 10 to 150 consecutive amino acids selected from the N-terminal end of human publicents lattogen (hBL), human growth hormone (hBL), prowth hormone variant (hGH V), or human growth peptides (hB) growth hormone variant (hGH V), or human prolactin, such peptides (h) inhibit capillary endothelal cell proliferation and organisation (ii) inhibit capillary endothelal cell proliferation and organisation (ii) inhibit least one specific receptor which describes not bind an intact full length hGH, hPL, prolactic or hGH-V. The invention also describes a method for diagnosing a probable absormatity of placental vascularisation during prequency. The poptides can be used for treating an anglogenic disease in a subject, for inhibiting tumour lormation or growth in a patient or for modulating vascularisation of a patient's placenta. In particular, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPPT1PLSRLFDNAMLRAHRIHQLAFDTYQEFERAYIPKEQKYSFLQNPQTSLSFSESIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant;
                                                                                                                New anti-anglogenic peptides - comprise N-terminal fragments of
numan placental lactoeen, human growth hormone, growth hormone
variant or human prolactin
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100.0%; Pred. No. 8.8e-40;
ive 0; Mismatches 0;
  Weiner RI;
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                                                                                                                                                                                                             Claim 4: Page 49-50: 87pp: English.
  faylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42861 standard; protein; 150 AA
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  Struman I,
                                              WPI: 1999-045192/04.
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es 92; Conserv
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                                                                    N-PSDB; AAXC1707
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Martial JA,
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AAY42861
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Figure growth cormone segment, used at the N-terminal of a fusion protein, which contains a thrombin recognition site, and human beta nerve growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91299).
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Pred. No. 3e-39;
0; Mismatches
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Best Local Similarity 98.9%;
Matches 91; Conservative C
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                                                                                           89EP-0102755
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(rirst entry)
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N-PSDB: AAN90269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-243092/34
                                                                                                                                                                                                                                                                            CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dementia, etc.
                                                                                                                                                                                                                                                                            HOSOL ( LEAT)
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                                                                                           17-FEB-1989:
                                                                                                                                                                                      19-FEB-1986;
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61-NOV-1989
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    23-AUG-1989.
                                                                                                                                                                                                                                                                                                                                                                       Ohtsuka E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sednouce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a chameric protein, which contains an N-terminal fragment of human growth hormone (h6H) of the sequence given in AAV42855, a cleavable peptide linker (AAV42857), and a human insulin precursor comprising insulin A and B chains (AAV42859). The h6H portion of the chimeric protein acts as an intranclecular chaperone (hKD) for the insulin precursor, enabling it to fold correctly. The cleavable peptide linker has a C-terminal Arg residue which enables the high portion of the chimeric protein to be removed after folding has taken place. Production of recombinant numan insulin with correctly inhed cystoine bridges with fewer necessary procedural steps, and mence resulting in a higher protein can provide himan insulin with correctly inhed cystoine bridges with fewer necessary procedural steps, and mence resulting in a higher protein can insulin. The INC sequences not only protein any approach is colubility of the fusion protein and decrease the intermolecular insulin sequences. From intracellular degradation by a microorganism isst, but also promete the folding of the fused insulin precursor. Facilitate the folding of the fused insulin precursor at commercially useful high concentrations. The reserve in the fused insulin precursor is commercially useful high concentrations. The sequence is the fused protein and decrease the intermolecular insulings and related purification science disvance of hydrophichte absorbent with a second containing the concentrations of nearcapten or the insect hydrophichte absorbent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPPTIPLSRLEDMAKLRAHBLACLARDTVORFBRAVIPKBOKYSBYGNPQTSLSPSBS1P +0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . HITT: HIT HITE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Match 150.0%; Score 470; 58.2%; Longth 150, Local Similarity 160.0%; Prod. Mo. 14-39; Coservative 6; Mismatches 0: Tudels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human growth hormone: fusion protein; thrombin;
geriatric dementia; nervous disorders; human nerve factor;
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                                                                                                                                                                                                                                                                                                                                                                       (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 30-31; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-610839/52.
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WO9950302-A1
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                                                                                               07-007-1999
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Matches
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DB 10; Length 146; 1; Indels

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Recombinant vector contg. fusion protein - consisting of human growth hormone or deriv. ligated to foreign protein, for stability and high yield.
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AA
                                                                                                                                                                     AAP90129 standard: protein: 192
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14-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, anti-anglogenic, prolactin; placental lactogen; hPL: anglogenosis; growth hormone; hGH: hGH-V: capillary endothelial cell proliferation; placental vascularisation; preparaty; treatment; anglogenic disease; tumour; inhibitor; malignant; anglofibroma; arteriovenous malicramation; arthritis; atherosclerotic plaques; corneal rate neovascularisation; wound healing; proliferative retinopathy; macular degeneration; trachoma; proliferative retinopathy; macular degeneration; trachoma; psychias; fibrojasia; solerodorma; kmposl's sarcoma; vascular adhesion; ulcer; leukaemia; reproductive disorder; contraceptive agent; adhesion; gene thorapy; pre-eclumpsia; intrauterine arowt; clardation;
                                                                                                                                                                                           2 MEDITIPLESRUEDNAMIRAHRIAGGAEDIYGEREANTPREGKYSELGNEGTSGSSESCOT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel human anti-angiotenic peptides derived from 10 to 150 consecutive amino acids selected from the N-termical end of human placental lactogen (MPL), human growth hormone (MGH), growth
                                                                                                                                                                                                                  1 MEPTIPLSRUFONAMURAHRINGLAFOTYGEFBEAYTPKEGKYSFLONPOTSLOFSESTP
                                                                                                                                                                     Silver Calva
                                The invention consists of a vector conty, a fusion protein which is formed by ligating, downstream of a promotor, mSH or a derive (proteinmed by subtstin.) of Mot-14 with lou) and a foreign protein. Stability of the vector in the host is greatly increased so the protein yield is higher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New auti-angiogenic peptides - comprise N-terminal fracments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human placental lactogen, human growth hormone, growth hormone variant or human prolactin
                                                                                                                                              Length 192:
                                                                                                                                                                     Indels
                                                                                                                                           Score 465, 28-16;
Pred. No. 4.28-39;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weiger Rig
                                                                                                                                                                                                                                                                                                                                                                                                     Human anti-angiogenic peptide hGH Met-1Phe191.
                                                                                             (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                          61 TPSNREETQQKSNLFLSLISLLSTQSWLEPVQ 92
                                                                                                                                                                                                                                                       HISTORIAN THEORY THE THE THE TEST TEST TEST TO SERVE PAGE 5.2
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                                                                                                                                                                                                                                                                                                                              AAW92264 standard: Protein; 192 AA
           Disclosure: Fig 1: 19pp; Japanese
                                                                                                                                             98WO-US09691.
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                                                                                                                                Guery Match
Rest Local Similarity 98.5.
Fine 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy, pre-ectoplacental dysfunction
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                                                                                                                     132 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martial JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1998.
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                                                                                                                     Sequence
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normal variant (naw, y), or numan protactin, such appliates (1) inhibit angiogenesis in chick choricallantoic membrane and (ii) binds to at least one specific receptor which does not bind an intract full, length city, prolactin or hGH-V. The invention also describes a method for diagnosing a probable abnormality of placental vascularisation during pregimency. The peptides can be used for treating an angiogenic disease in solubect, for inhibiting tumour formation or growth in a patient or for medulating vascularisation of a patient's placenta. In particular, the peptides can be used for treating e.g. malignant tumours, regional and vascularisation of aptent's placenta. In particular, the peptides can be used for treating e.g. malignant tumours, regional and real placents, anderesolatoric plaques, corneal grathitic such as rheumatoid artifitis, atherosolatoric plaques, corneal grathitic such as rheumatoid artifitis, atherosolatoric plaques, corneal grathitic such as those occurring of a trivitis, anderesolatoric plaques, corneal grathitic such as those occurring to relinopathy, macuiar degeneration, granulations such as those occurring such as hyportrophic scars or keloid scars, neovascular glaucoma, ocular timent, uveling macuiar degeneration, granulations such as those occurring such as hyportrophic scars or keloid scars, neovascular glaucoma, retrolental fibroplasia, scleroderma, solid tumours, kaposi's sarcoma. Trachoma, vascular adhesions, chronic varicose ulcers, neovalis the peptides can also be used as contraceptive agents of such development associated with pre-ediampsia, intrautering growth retardation, and placental can be used in assays for impairment of vascular development associated with pre-ediampsia, intrautering growth retardation, and placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFPTIPLSRIFONAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone variant ({\rm HGH-V}), or human prolactin. Such peptides (i) inhibit capillary endothelial cell proliferation and organisation (ii) inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human nerve growth factor and human growth hormone fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.9%; Score 465; DB 20; Longth 192; 98.9%; Pred. No. 4.2e-39; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human merve growth factor; fusion protein; thrombin; qeriatxic dementia; nervous disorders; human growth hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 91, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 AA;
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1 MFPTIPLSKLFDNAMLRAHRLHQLAFDTYQEFFRAYIPKEGKYSFLONPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The protein is produced by fusing DNA encoding BDF (IL-) with DNA encoding BSF-2 (IL-5) and ligating the product into an expression vector Sec also AAR05311 and AAR05313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEPTIPLSRLFDNAMERAHRIHQLAFDTYGEFEEAYIPKEQKYSFLONPQTSLSFSESIP
                                                                                                                                                                                                                                                                                                                                                                        5-cell stimulatory factor-2; interleukin-6; B-cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prepn. of human B-cell differentiation factor - from specified sequence segment, by recombinant DNA technique, gives protein o specified amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.9%; Score 465; DB 11; Length 310; 98.9%; Pred. No. 7.3e-39;
                         Length 262;
                                                                                                                                                                                                                                                                                                                              Fusion protein of B-cell stimulatory factor-2 and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                         98.9%; Score 465; DB 12;
98.9%; Pred. No. 5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TPSNREETQOKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                         61 TPSNREETQQKSNLHLLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 31; Page 9; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR05313 standard; protein; 144
                                                                                                                                                                                                                                            AAR03255 standard; protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                      interleukin-5; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88JP-0162556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88JP-0162556,
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                             differentiation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-062207/09.
N-PSDB; AAQ02028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                       Local Similarity
hes 91: Conserv
262 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               JP02013375-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1990.
                                                                                                                                                                                                                                                                                                   19-JUL-1990
                                                                                                                                                                                                                                                                        AAR03255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
best Local &
apuonbas
                            Chery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR05313
ID AARC
XX
                                                                                                                                                                                                                 RESULI 9
                                                                                                                                                                                                                                AAR03255
                                                                                                                                                                                                                                                           33
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                                                                                                                                                                                                                                                                                                     ä
                                                                                                                        Fusion protein consisting of human growth hormone at the treminal end (1st region), a 3 amino acid sequence representing thrombin recognition site, and human beta nerve growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatus demontia and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91041).
                                                                                                                                                                                                                                                                                                                                1 MEPTIPLSKLFDNAMLRAHRZHQLAPDIYGEFEEAYIPKEGKYSFLCNPQISLSFSSSIP 60
                                                                                                                                                                                                                                                                                                                                               A recombinant human nerve growth factor beta subunit-contg, protein can be produced as this fusion protein. It is purified by contacting a gel having a cation exchange gp, with the fusion protein, in the presence of urea. The purified protein is useful in a medicament for treating disorders of the nervous system, eg dementia.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                     90.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purifica, of human neuron growth factor beta-subunit-contg, prutein by contacting with gel having cation exchange gp, in presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human growth hormone/human nerve growth factor beta fusion protein
                                       New human nerve growth Lactor game encoding tuston protein - having cleavage site for thrombin, useful for treating geniatric
                                                                                                                                                                                                                                                                                                     ċ
                                                                                                                                                                                                                                                                        Score 465: DB 10; Length 261; Pred. No. 6e-39:
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                     hGH; hNGF; nervous system diseases; dementia
                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                 Claim 36; page 31-32; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11740 standard: Protein; 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure ; fig 1; 7pp; Japanese.
                                                                                                                                                                                                                                                                        98.98;
98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89JP-0202835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89JP-0202835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                                                                      Best Local Similarity 98.9
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPT: 1991-128768/18
            1989-243392/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                             261 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ11578.
                                                                        dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP03067598-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR11740:
                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                        Query Match
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CHERY Match
Best Local Similarity
Think 90; Conserva
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N-PSDB; AAN81605.
                      WPI; 1986-281696/43
                                                                                                                       Sequence 262 AA;
       (CTSU/) OTSUKA E.
                                                                                                                                                                                                                                                                                                                       Grewth hormone
                                                                                                                                                                                                                                                                                                                                                    JP63167798-A
                                                                                                                                                                                                                                                                                                                                                                                 29~DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                29 - DEC - 1986;
                                                                                                                                                                                                                                                                                 25-MAR-2003
20-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                  11-JJL-1988
                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                  AAP81226,
                                                                                                                                                                                                                                             AAP81226
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                                                                                                                                                                                                                     The sequence encoding this protein can be fiscal with ENA encoding B util differentiation factor (ii-6) and ingated into an expression vector for producing a fusion protein. See also AARSSII.
                                                                                                                                                                                                                                                                                                       1 MFPTIPLSRLFDNAMLRAHRIHQLAFUTYQEFEEAYIPKEQKYSFLONFQTSLSFSFSIP 60
                                                                                                                                                                                                                                                                                                               Gans
                                                                                                                                                                        Preph. of human H-cell differentiation tactor—from specified INA sequence segment, by reconstrant DNA technique, gives protein of specified amino acid sequence.
                                                                                                                                                                                                                                                                          Sength 144;
                                                                                                                                                                                                                                                                                        1: Indels
                                                                                                                                                                                                                                                                        Score 462; DB 11;
Pred, No. 6.1e:39;
                             Segment of B-cell stimulatory factor-2 (IL-5).
                                                                                                                                                                                                                                                                                                                                     61 IPSNREBIOOKSNLELLRISLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                            Human beta-nerve growth factor gene product
                                           B-cell stimulatory factor-2: interleukin-5.
                                                                                                                                                                                                                                                                                       : Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
145..262
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                                                                                                                                                                                                      Disclosure, Page 9, 17pp, Japanese
                                                                                                                                                                                                                                                                        98.3%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85CP-0045773.
                                                                                                       88.312~016.255%.
                                                                                                                     38JF-016255:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85JP-0045773
                                                                                                                                                                                                                                                                                                                                                                                        AAP61033 standard; Protein;
              19-JUL-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 97.8*
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-NGF; E.coli; ds
                                                                                                                                                   1990-062207/09
                                                                                                                                   (TOYE ) TOSCH CORP.
                                                                                                                                                                                                                                                          144 AA;
                                                                                                                                                          N-PSDB; AAQ02028
                                                                         JP02013375-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP61205485-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1985;
                                                           Homo sapiens
                                                                                                                     01-JUL-1988;
                                                                                                      01-331-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     25-0CT-1991
                                                                                        17-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-1986
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       AAP61033;
AARC5313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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ID AAP6
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The polypeptide (AAPB1226) with somatomedin-like activity and the DNA (AANB1605) encoding it are claimed. A Met resicual qp. may be added to the W.terminal. The polypeptide acts on the hone structure of mammals, including humans, to promote bone growth. The polypeptide has high production rate and is casily extracted from bacterial culture medium and refined for use as a bone growth accelerator. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                 The protein is a direct translation of the upstream tryptophan promoter-operator lacking its attenuation sequence and human abder-NGF sequence. The product may be efficiently expressed from a transformed E.coli expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                    ..
  jc
                                                                                                                                                                                                                                                                                                                                                                Length 252;

    used in prodn.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of protein with somatomedin-like activity.
                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                          98.3%; Score 462; DB 7; 97.9%; Pred. No. 1.2e-38; ative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene segment of human nerve growth factor - WSF-producing recombinant Escherichia strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2(1); Page 609; 9pp; Japanese.
                                                                               Claim 32: Page 482: 71pp; Japaneso.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP81226 standard: protein; 138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86JP-0310177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86JP-0310177.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Detection; fluoresce: illegal misuse; growth substance; athlete; domesticated farm animal; cattle; human growth hormone.
                                                                                                                                          Frimary amine acid sequence of native human growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of tagged exogenous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 1, 38pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENERIC BIOLOGICALS LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-GH03449
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkinson A, Murphy JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-338072/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :91 AA;
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6-NCV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JJN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                        28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         27 - MAY - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY04396;
          AAY15809,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rest Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARY04396
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                                                                                                                                                                                                                                    2 FPTIPISRLFONAMLRAHRUHQLAFDTYOBFBFAYIPKFÖKKSFLUNPOISLSFSESIFT 6. HILLILLILLI HILLI 
                                                                                                                                                                                              2 FPTIPLSRLFDNAMLRAGRUHQLAFDTYORFERAYIFKEGKYSFLONFOTSLSFSESTPT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Syndroc.
Cormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a secum albumin-growth hormone fusion professionaseful to treat growth hormone related diseases such as nown's syndrome. This sequence represents a protein of the serum albumin-greath hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serum albumin-growth hormone fusion protein - useful to treat growth hormone related diseases, e.g. Down's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%: Score 460: DB 19: Length 191: 98.9%: Pred. Nc. 1.30-38: 1.06: 8: 1.30-38: 1: 1ndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serum albumin-growth hormone fusion protein; growth hormone:
                                                                 Score 460; DS 9; Length 136:
Prod. No. 9.46-39;
0: Mismatches [: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             racers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein sequence of the hGH growth hormone cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSNREETQQKSNLELCRISLLSIQSWLEPVO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSNREETOOKSNLELLRISLLITOSWLEPVO 91
                                                                                                                                                                                                                                                                                                                                     62 PSNREETQQKSNLELLRISHLIOSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                    PSNREETQQKSNLECLRISLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA020116 standard: Protein: 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY15809 standard; protein: 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Fig 1, 21pp; Korean.
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                                                              Cuery Match
Best Local Similarity 98.98;
Matches 90; Conservative
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3.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     administered substance from a method of detecting an exogenously administered substance from a naturally-occurring endogenous substance the exogenous substance being tagged so that it fluoresces differently from the endogenous one at a suitable wavelength. The tagging may consist of one or more substitutions in tagged growth hormone selected from 340V, 52V, w86F, Y, L, I or V P103Y or 1137Y. The method is used to distinguish between exogenously administered substances as compared to naturally-occurring endogenous substances. Especially menthoned is the integral manually exogenous substances by attlactes or in domesticated farm animals e.g. cattle. The present sequence represents mainly forwith hormone which may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 FPT1FLSRLFDNAMLRAHKLHQLAFDTYQEFBEAYIPKEQKYSFLONPQTSLSFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 22kDa growth hormone; hGH; mutant; thrombin; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Match 97.9%; Score 460; DB 20; Local Similarity 98.9%; Pred: No. 1.3e-38; es 90; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 PSNREETQOKSNIELLRISHLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSNREETQQKSNJELLRISHLIHILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natural human 22kDa growth hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY04396 standard; protein; 191
                                                                                                                                                                                                                                                                                                     the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmin; decomposition.
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06-APR-1999

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The present invention describes a human arowth housone mitten is which the 134th Arg and the 135th Thr are replaced respectively by Asp and Brothn the 15 to the 191st amino acid sequence in thatural type human 22 king growth hormone (Adi) and which has a resistance analyst decomposition by thrombin. The present sequence represents the natural BSH. Also and the 143th Lys are replaced respectively Asp. Pro and A.a in the amino acid sequence of matural type hill and which has a resistance amino acid sequence of matural type hill and which has a resistance against decomposition by thrombin and plasmin; and (2) a ding preparation containing the above holl mand as the active component. The mutant hill shows an activity approximately expiration to that of natural type hill and shows a high stability in blood and body finid.
                                                                                                                                                                                                                            A human growth hormone mutable with equivalent activity to natural human growth hormone
                                                                                                                                                                                                                                                                                      Example 1; Page 5:6; 10pp; Japanese.
                                                                                                    97JP-0275277
                                                           97JP-0275277
                                                                                                                                             (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                      WPI; 1999-283567/24
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                                                           22-SEP-1997;
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5000 frdels 0: 62 PSNREETQCKSNLEELRISTLIOSWLEFVO 92 F. HILLE HILL HILL HILL HILL HILL HILL FILL GSWLEFVO 91 FSNREETQCKSNLEELRISTLLIQSWLEFVO 91 Ouery Match Best Local Similarity 99.99 Matches 90, Conservative qq ò ò

Search completed: September 15, 2003, 12:00:57 Job time: 65.6308 secs

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                                                       September 15, 2003, 11:57:46 : Search time 21.1599 Seconds (without alignments) 184.449 Million cell updates/sec
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Sequence 12.
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Sequence 24.
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                                                                                                                  1 MPPTIPLSRLFDNAMLRAHR......NLELLRISHLLIQSWLEPVQ
                                                                                                                                                                                                                                                                                     1: /cgn2_6/ptodata/1/iaa/5A_COMH.prp:*
2: /cgn2_6/ptodata/1/iaa/5#.COMH.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMH.pep:*
4: /cgn2_6/ptodata/1/iaa/6#.COMH.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMH.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMH.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Computer, 2545.
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US-09-422-819-37
US-09-422-819-37
US-08-800-2:5C-18
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05-08-784-582-10
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US-08-469-486-51
US-08-469-658-51
US-08-710-324A-4
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US-08-459-906-4
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                                                                                                                                                                    328717 seqs. 42310858 residues
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                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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	ALIGNMENTS					
Sequence I, Appli	JS-07-922-523-1	-	<u>.</u> .	63.7	239.2	⊕
m.	-62-69-		<u>ာ</u>	63.7	299.5	44
	US-09-105-651-3	7	216	64.1	301.5	43
	US-08-459-906-1	'n	193	64.1	301.5	42
Sequence :, App	US-08-383-621-1	7	193	64.1	301.5	4
	US-08-363-982-2	_	193	64.1	301.5	0.4
ć	US-67-621-197C-2	1	163	64.1	301.5	5£
	5210186-1	c	<u>.</u>	64.1	301.5	38
5,	US-09-277-720-2		190	64.1	301.5	3.7
(1	US-08-388-267C-2		190	64.1	301.5	36
Sequence i, App	US-09-105-651-1		216	64.4	302.5	35
÷	US-07-963-331D-4		5.	64.8	304.5	34
∞`	US-08-458-824-8		131	65.2	306.5	33
Ŋ	US-09-411-657-5	7	198	71.0	333.5	4.5
'n	US-08-71C-324A-5		138	71.0	\$33.5	, ; ; ~,
	US-08-187-756C-5	_	 & &	0	553.5	(0.8
Patent No. 54241	5424199-3		168	72.3	0.45	52
Sequence 2, Appli	US-08-990-774-2		175	76.4	\$58.5	28

DNA for Expression of Bovine Growth Hormone COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: patin (Generitoch)
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093.383
FILING DATE: 14-JUL-1993
CLASSIFICATION NUMBER: US/08/19827
FILING DATE: 28-NCV-1990
FRIOR APPLICATION NUMBER: 07/198824
FILING DATE: 28-NCV-1990
FRIOR APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1986
FRIOR APPLICATION NUMBER: 06/632361 APPLICANT: Seburg, Peter H.
TITLE OF INVENTION: DNA for Expression NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California 06/303687 APPLICANT: Heyneker, Herbert L. NAME: Johnston, Sean A.
REGISTATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 46C4
TELECOMMUNICATION INFORMATION: FILING DATE: 19-501.-1984 PRIOR APPLICATION ISATA: APPLICATION NUMBER: 06/30 FILING DATE: 16-SEP-591 ATTORNEY/AGENT INFORMATION: 94080

TELEA: 415/952-9881
TELEX: 910/371-7168
INFORMATION FCK SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids TYPE: amino acid

Appli Appli

Sequence Sequence 2

US-08-791-728-1 US-08-950-774-1 US-08-791-728-2

Sequence

IELEPHONE: 415/225-3562 IELEFAX: 415/952-9881

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APPLICANT: Delay, Michael J.
APPLICANT: Buckwaiter, Brian L.
APPLICANT: Cady, Susan M.
APPLICANT: Cady, Susan M.
APPLICANT: Shich, Hong-Ming
APPLICANT: Bohlen, Peter
3.17LE OF INVENTION: Stabilization of Somatotropins and Other
TITLE OF INVENTION: Proteins by Modification of Cysteine Residues
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%; Score 466; DB 2; Length 194;
98.9%; Pred. No. 6.1e-51;
live 0; Mismatches 1; Indels
                                                     COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPATIBLE
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRAL APPLICATION DATA:
APPLICATION NUMBER: US/08/385,621
FILING DATE: C6-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Mismatches
                                                                                                                                                                                                                              CLASSIPICATION: 514
PROCK APPLICATION DATA:
APPLICATION NUMBER: 08 07/766,142
ATTCRNBY/AGEN: 1N°ORMATION:
NAME: TSCA'DOS, SECELLE C.
RECISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,278-01
TELEPHONE: 203-321-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: American Cyanamid Company STREET: one Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s Sequence 4, Application US/08459906
patent No. 6010999
                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 203-710-474-4059
INFORMATION FOR SEQ 15 NO: 4:
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FILING DATE: C2-JUN-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 194 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rest Local Similarity 98.9
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: New Jersey
FRY: U.S.A.
07470-8426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wayne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Olazaran, Martha Guerroro
APPLICANT: Saldana, Horo Barrera
ITTLE OF INVENTION: Genetically Modified Methylographic P. pastoris Yeast Ital Colnymin (Constant Applicant) Barrera (Constant Applicant A
                                                                                                                                                                                                                                          1 MEPTIPLSRLFDNAMLRAHRIHGLAFDTYOEFBEAYTPKECKYSFLONPOTSLSFSESIP 60
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(0.00)
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TILE OF INVENTION: Stabilization Of Somatotropins And Other
TILE OF INVENTION: Proteins By Modification of Cysteine Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
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                                                                                          Length 1927
                                                                                                                                                   1; ludels
                                                                                       Score 465: DB 1:
Pred. No. 1.4e-51;
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1937 West Main Street, P.O. Box 60
                                                                                                                                                                                                                                                                                                                               61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                              61 TPSNREETOCKSNLEEERISEELIQSWLEEVO 92
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                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09284878
Patent No. 6342375
GENERAL INFORMATION:
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Patent No. 5951972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APFIJCANT: Dalcy, Michael J.
APPIJCANT: Buckwaller, Brian L.
APFIJCANT: Gady, Susan M.
APPIJCANT: Shieb, Hong-King
APFIJCANT: Boblen, Peter
                                                                                    98.98
98.98
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Best Local Similarity 98.9%
Final 90; Conservative
                                                                           98.91
Best Local Similarity 98.91
Matches 91; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-284-878-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Stamford
STATE: Connecticut
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06904-0060
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STREET: 19
TOPCLOGY:
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SEQ ID NO 5
LENGTH: 19:
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US-08-693-383-
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ICPOLOGY:
US-08-784-582-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Newgard, Christopher B.
APPLICANT: Halban, Philippe
APPLICANT: Halban, Philippe
APPLICANT: Clark, Samuel A.
APPLICANT: Triagen, Anice E.
APPLICANT: Ruse, Fred
TITLE OF INVENTION: Recombinant Expression of Proteins From ITLE OF INVENTION: Secretory Coll Lines
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AFROIG, White & Dirkee
STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                           97.9%; Score 460; DS 3; Length 194;
98.9%; Pred, No. 6.1e-51;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: ISM FC compatible
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-10.5/MS-DOS
SOFTWARE: Patentin Release 41.6, Version 41.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/68/589.028
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGNIT INFORMATION:
NAME: Bighlander, Sleven D.
REG-STRATION MINNER: 47,642
REFERENCE/DOCKET NUMBER: UTSE:426\HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3(00
                       31.278-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08589028 Patent No. 6087129
               REFERENCE/POCKET NUMBER: 31.2
TELECCHMULCATION INFORMATION:
TELEFROM: 201-83:3247
TELEFAX: 201-83:3305
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 aming acids
REGISTRATION NUMBER: 34,276
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
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amino acid
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.33
Matches 90, Conservative
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                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy:
                                                                                                                                                                       amino acid
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US-08-589-028-10
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97.9%; Score 460; DB 3; Length 217;

Query Match

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                                                                                                                                                 2 FPTIPLSRLFUNAMLKAHRLHQLAFDTYQBFEEAYIPKEQKYSFLQNPQTSLSFSESIPI
                                                           Gaps
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APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: Clark, Samuel A.
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: McGarry, Demnis
APPLICANT: McGarry, Demnis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM NUMBER OF SEQUENCES: 79
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                                                           Indels
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CCMPUTER: IN PC Compatible
CPERAING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.30
    98.9%; Pred. No. 7.1e-51; ve. 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                     62 PSNREETOUKSNLELLRISLLLIQSWLEPVQ 92
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FILING DATE: Concurrently Herewith
CLASSYPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 68/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10. Application 05/08784582
Patent No. 6110707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0:
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Best Local Simitarity 98.9%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.9
Matches 90; Conservative
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MEDIUM TYPE: Floppy
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2.Tp: 77210
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2 FPTIPLSKLFUNAMLRAHRLHQLAFOTYQEFFEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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APPLICANT: ROCK, Fernando I.,
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TILLE CF INVENTION: MUTATIONAL VARIANTS OF MAMELIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 217;
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Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 192.210
OTHER INFORMATION: /ncte- "The peptides above are
OTHER INFORMATION: depicted in Figure 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHWARE: Patentin Release #1.0, Version #1.36
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILLNG DATE: 05-DEC-1996
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                                                                                                                  STREET: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Aito
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
FRIOR PAPLICATION: 435
FRICA ATTON ROBER: 05 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chicq, Edwin P.
RESISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olazaran, Martha Guerrero
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-284-678-1
7 Sequence 1, Application US/09284878
Fatent No. 6342375
GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: DOTELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IELEPHONE: 415-812-9196
TELEFAX: 415-496-1200
INFORMATION FOR SRC ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 217 amino acids
amino acid
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Best Local Similarity 96.99
Matches 90; Conservative
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PEATURE:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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133..153
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32..53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                      APPLICANT: Newgard, Christopher H.
APPLICANT: Newgard, Philippe A.
APPLICANT: No. 5194176minaton, Karl D.
APPLICANT: Clark, Samuel A.
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Christ, an
APPLICANT: Kruse, Fred
TITLE OF INVENTION: RECOMMINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 460; DB 3; Jenuth 217; 98.9%; Pred. No. 7.1e-51;
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                                 62 PSNREETQQRSNLELLRISLLIQSWLEPVQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
lBM PC compatible
SYSTEM: PC-NOS/MS-DOS
                                                                                                                                                                                                       Sequence 10, Application US/33785271
Patent No. 6194176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/38759628
; Patent No. 6225446
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 217 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 15M PC of OPERATING SYSTEM:
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Best Local Similarity
Matches 90; Conserv
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APPLICANT: Newgard
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CIIY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Texas
COUNTRY: USA
ZIP: 77210
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QO ò D, S

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GENERAL INCOMARTION:
APPLICANI: Sato, Seiji
APPLICANI: Sato, Seiji
APPLICANI: Higashivituki
APPLICANI: Kudo, Toshiyuki
APPLICANI: Kudo, Toshiyuki
APPLICANI: Kudo, Toshiyuki
APPLICANI: Kondo, Masaaki
TITLE OF INVENTION: DREPARING USEFUL POLYPEPTIDES IHROUGH EXPRESSION OF THE
TITLE OF INVENTION: DRAS
FILE REFERENCE: 382-1026
CURRENT APPLICATION NUMBER: US/09/286,036A
CURRENT APPLICATION NUMBER: JP10-87339/1998
EARLIER FILING DAFE: 1999-03-26
EARLIER FILING DAFE: 1998-03-16
NUMBER: PATENTING OFFE: 1998-03-16
                                             | HILLSTOTH | HILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Designated is OTHER INFORMATION: an amino acid sequence of MWPsp-MWPmp20-TEV-G-GH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 460; DB 4; Length 245; 98.9%; Pred. No. 8.4e-51; Indels Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                               Segmence 66, Application US/0928003GA
Fatent No. 6506595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71. Application US/08784582 Patent No. 6110707
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Best Local Similarity
Matches 90, Conserv
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ZIP: 77210
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LENGTH: 245
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                                                              TILE OF INVENTION: Genetically Modified Methylatrophic F. pastoris Yeas, for the III E OF INVENTION: Broadcation and Scoretion of the Buran Growth Brimman FILE REPERENCE: 1829, 0510000 CURRENT APPLICATION NUMBER: US/09/284,878 CURRENT APPLICATION NUMBER: US/09/284,878 CURRENT APPLICATION NUMBER: PCT/KM99/20039 PRIOR FILIUG DATE: 1999-07-21 PRIOR FILIUG DATE: 1997-10-24 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.1 SEQ ID NOS: 9
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INVENTION: Process for preparing recombinant procedus using highly
efficient expression vector from Sucharcmyces cerevisiae
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CORRESPONDENCE ALDRESS:
ADDRESSEE BACHAN 5 TAPOINTE, P.C.
STREET: SOLICE 12G1, 900 Chapel Street
CITY: New Haven
STATE: Connecticut.
COUNTRY: U.S.A.
ZIP: 05510-2802
COMPUTER READABLE FORM:
MEDIJW TYPE: DISSECTE, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 460; DB 4:
Pred. Nc. 7.1e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 PSNREETQQKSNLELLRISLLIQSWLEPVQ 117
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APPLICATION NUMBER: US/09/424,6205
FILLING DATE: 24-403, 6791585-1999
INFORMATION FOR SEQ 1D NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PSNRRETQQKSNLELLKISLLLLQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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OPERATING SYSTEM WINDOWS 95/98
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GS-09-424-6208-25
Saldana, Hugo Burrera
Salvado, Jose Maria Viador
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09424620B Patent No. 6391585 GENERAL INFORMATION:
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YANG, Doo-Suk
LEE, Jee-Won
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOON, Jae-Woong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JANG. Ki-Ryong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%;
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Best Local Similarity 98.9
Matches 90; Conservative
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Best Local Similarity 98.9
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-878-1
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US-09-424-620B-25
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                                  APPLICANT:
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LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 73, Application US/03784582
Patent No. 6110707
GENERAL INFCRMATION
FAPLICANT: Newdard, Christopher B.
APPLICANT: No. 6110707mington, Karl D.
APPLICANT: Olark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Unade, Christian
APPLICANT: Unade, Christian
APPLICANT: Wadade, Christian
APPLICANT: Wadade, Christian
APPLICANT: Wadade, Christian
APPLICANT: Wedarty, Desnis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
ITHER OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sength 274,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%: Score 460: DP 3: Length 274
98.9%: Pred. No. 9.9e-51;
Wismanches 1: midels
                MEDIUM TYPE: Floppy disk
CCMPUTER: 1BM PC COMPALIDIA
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.6, Versich Fl.30
CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.2, Vorsion #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                              NAME: Highlander, Stevel L.
REGISTRATION NUMBER: 37,642
REFERNOE/DOCKET NUMBER: UTSD:514
IELECOMUNICATION INFORMATION:
TELEPRONE: 512/418-3000
INFORMATION FOR SEQ ID NO: 71;
SEQUENCE CHARACTERISTICS:
LENGIH: 274 amino acids
                                                                                                                   APPLICATION NUMBER: US/28/784,582
FILING DATE: CONGULTERLLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Box 4433
CITY: Houston
STATE: Revie
                                                                                                                                                                                                                                              FILLING DATE: 19.7AN-1995
ATTORNEY/AGBNT INFORMATION:
                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 50/028,427
FILING DATE: 15-0CT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 38/589,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/784,582
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.9%
Thes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSE: Arnold, W
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: lisear
US-08-784-582-71
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APPLICANT: CHAPPEL, SCOtt
TITLE OF INVENTION: Human Growth Hormone to stimulate hematopoiesis and immune:
TITLE OF INVENTION: Human Growth Hormone to stimulate hematopoiesis and immune:
TITLE PERSENCE: Affappel=6.
CURRENT APPLICATION NUMBER: US/09/465,461
PRIOR APPLICATION NUMBER: 60/112.17
PRIOR APPLICATION NUMBER: 60/112.668
PRIOR FILING DATE: 1998-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : FPTIPLSRLFDNASLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FPTIPLSKLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEGKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FPTIPLSRLFDNAMLKAHRLEQEAFDTYQFFEEAYIPKEQKYSFLONPUTSLSFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%; Score 460; DB 3; Lv
98.9%; Pred. No. 1.46-50;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 454; DB 4;
Pred, No. 3.5e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
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           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 060/028,427
FILING DATE: 15-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 080/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
Concurrently Herewith
                                                                                                                                                                                   NAME: Highlander, Sleve: L.
RESISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
TELEPHONE: 512/4 UB-3009
TELEPHONE: 512/4 UB-3009
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Patent No. 634844
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
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                                                                                                                                                                                                                                                                                                                                                           LENGTH: 350 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.81
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin ver
SEC ID NO 1
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Best Local Similarity
Matches 90: Conserv
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US-08-784-582-73
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US-09-465-461-1
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2 FPTIPLSRLFDMAMLBAHRUEGJAFOTYOEFERAYIPKROXYSFLGMEGTSLSFSRIFT (1 1 111 1 111 1 111 1 111 1 111 1 111 27 FPTIFLSRLFDMASLRAHRLHGJAFDTYOEFERAYIFKHGAYSFLGMEGTSLGFSESHITT 66
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Best Local Similarity 97.8%; Pred. No. 4.26-50;
Matches 89; Conservative 6; Mismatches 2; Indels 6; Gaps
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSEN, ET AL.
TITLE OF INVENTION: Himman Growth Hormone
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: GRECKEL, STEWART & GLSTEIN
STREET: GRECKEL FARM RAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: CSA
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MEDIUK TYPE: 3.5 INCH DISKETTE
CCMPUTER: 18 PS/2
OPERATING SYSTEM: MS-DDS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187/756C
ILNG DATE: January 27, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 12 PS PRIOR APPLICATION NUMBER: ELING DATE: APPLICATION NUMBER: STATE
ATTORNEY AGENT INFORMATION:
WAME: FERRARO, GREGORY D.
HEGISTRATION NUMBER: 325800-55
FILEDHOME: 201-994-174
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 AMINO ACID
STRANDEDNESS:
TYPE: AMINO ACID
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINBAR
WOLFCULE TYPE: PROTEIN
US-68-187-756C-4
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Search completed: September 15, 2003, 12:05:31 Job time: 22:1639 secs ó qq

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Sequence 2, Apr. 2, Sequence 23, Apr. 3, Sequence 23, Apr. 1, Sequence 2, Apr. 1, Sequence 6, Apr. 1, Apr. 1, Sequence 6, Apr. 1, 
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847.945 Millios cell uplates/sec
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                                                                                                                                                                                                                                                                                                                    September 15, 2063, 12:03:35 ; Search time s6,5905 Seconds
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2: /cgn2_6/ptodata/1/pubpaa/USG7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USG5_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USG5_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USG5_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USG3_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodata/1/ptodat
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/cgn2_6/ptodata/!/pubpaa/US10C_PUBCOM6.pep.*
/cgn2_6/ptodata/!/pubpaa/US10_NBM_EUR.pep.*
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Gendere version 5.1.6 dopyright (d) 1993 - 2003 compages that.
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108-10-054-073-7

108-09-984-010-23

108-10-153-207-1

208-10-153-207-1

208-10-10-123-207-1

208-10-10-123-207-1

208-10-123-207-1

208-10-123-207-1

208-10-123-207-1
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US-09-853-688-2
US-09-969-748C-4
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US-09-850-887-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                               OM protein - protein search, using swindel
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Gapop 10.0 , Gapext 0.5
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1 MEPTIPLSREEDNAMERAHR.
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 350, App	Sequence 2, Appl	Sequence 411, App				-									•				٠,	٠.		• •	•					Sequence 4, Appli	Sequence 20, Appl
US-10-643-487-350	US-10-153-207-2	US-10-103-313-41;	US-10-188-246-18	US-10-153-207-3	US-10-054-873-1	US-10-054-873-6	JS-10-191-879-19	US-10-191-879-10	US-10-043-487-337	US-09-887-569A-2	US-10-322-746-4	US-09-876-478-14	US-10-140-293-32	US-10-140-293-33	US-10-140-293-26	US-10-140-293-27	US-10-140-293-31	US-10-140-293-22	US-10-140-293-21	4 US-10-036-869-25	6	69-2	93-2	93-1	93	93-1	US-10-140-293-13	US-10-153-207-4	US-10-140-293-20
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ALIGNMENTS

APPLICANT: Gan, Zhong Ru IITLE OF INVENTION: Chimeric Protein Containing an Intramblecular Chaperone-Like Sequence

NUMBER OF SECUENCES:

Sequence 2, Application US/10054873 Publication No. US20020164712A1 GENERAL INFORMATION: APPLICANT: Gan, Zhong Ru

US-10-054-873-2

CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Mabarcadero Center, Highth Floor CITY: San Francisco STATE: California

COUNTRY: USA

ZIP: 9411-384
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC COMPALIBLE
COMPATION: SYSTEM: PC-NOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

NAME: Mycroft, Frank J REGISTRATION NUMBER: 46,946 FFERENCE/DGCKET NUMBER: 020167-060136US INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 92 amino acids IYPE: amino acid

APPLICATION NUMBER: WO PCT/CN98/00052 FILING DATE: 31-MAR-1998 APPLICATION NUMBER: US 09/423,100 FILING DATE: 11-DEC-2000

ATTORNEY/AGENT INFORMATION:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2602
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:

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6) TPSNREETQQKSNLELLRISHLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                            STATE: DC
COUNTRY: USA
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nes 90; Conserva
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US-09-984-010-23
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Rest Local S:
Matches 90,
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GENERAL INFORMATION:
APPLICANT: Gan, Zhoma Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramplecular Chapperone Like Sequence
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                                                                                                           100.0%; Score 470; DB 14; Length 32; 106.0%; Pred, No. 2.2e-46;
                                                                                                                                                Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054.873
FILING DATE: 22-Jan-2002
CLASSIFICATION: <CORNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Traw LLF
STREET: Two Embarcadero Conter, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: WO PCT/CN98/00552
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEG-2006
AITORNEY/AGENT INPORMATION:
NAME: Mycroft, Frank U
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167.030130US
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                      61 TPSNREETQQKSNLELLRISLLLQSWLEPVQ 92
                                                                                                                                                                                                                                                                         61 TPSNREETOOKSNLEIGRISELLIOSWEEPVO 92
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                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-654-873-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TRM FV COMPUTER:
                TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: US-10-054-873-2
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publication No. US20020164712A1
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STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
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                                                                                                                            Best Local Similarity 100.0
Matches 92; Conservative
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Best Local Similarity
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                                                                                                           Query Match
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Sequence 23. Application US/09984Cl0
Publication No. US20C30154578Al
GENERAL INFORMATION:
APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: FINNECAN, HENDERSON, FARABOW, GARRETT & DUNNER,
STREET: 1300 I Street, NW
                                                                                                                                                                                                                                                                                                                     COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984.01C
FILING DATE: 21-May-2002
PRICH APPLICATION NUMBER: US 09/091.873
APPLICATION NUMBER: US 09/091.873
FILING DATE: 25-JUN-1998
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 19-DEC-1996
INFORMATION FOR SEC, 13 NO: 23 :
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amitio acids
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Publication No. US200301530331
GENERAL INFORMATION:
APPLICANT: James A. Wells
TITLE OF INVENTION: GROWTH HORMONE VARIANTS
FILE RFFERENCE: 669-12-US-C7
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT FILING DATE: 2002-05-22
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                                                                                                                              AND SERUM ALBUMIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 06/479,884
PRIOR FILING DATE: 1995-66-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYPE: amino acid
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Indels

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2 FPTIPLSRLFDNAMLRAHRLHOLAFDTYQEFEEAYIPKEQKYSFLCNPQTSLSFSESIPT
                                                                                                                                                                                                                                                                                     Score 460; DB 12; Length 191; Pred. No. 7.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6. PSNREETQOKSNLELLRISLLLIQSWLEPVQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 PSNREETQUKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                            0; Mismatches
CURRENT APPLICATION NUMBER: US/10/466,708
CURRENT FILING DATE: 2603-63-26
FRIDR APPLICATION NUMBER: US/09/462,941
PRIDR FILING DATE: 2000-01-14
PRIDR FILING DATE: 1997-07-14
FRIDR FILING DATE: 1997-07-14
                                                                                                                                                                                                                                                                                     97.98;
98.98;
                                                                                                                                                                                                                                                                      Ouery Match
Hest Local Similarity 98.9%
Withmas 90; Conservative
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                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 90: Conserv
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US-10-153-207-6
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                                                                                                                                                              SEO ID NO 1
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APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10406377
Publication No. US2033016294941
GENERAL INFORMATION:
APPLICANT: COX III. George N
APPLICANT: Boider Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins:
FILE REPRENCE: 4152-1-108
CURRENT APPLICATION NUMBER: US/10/4400, 377
CURRENT PILING DATE: 2003-03-26
PRIOR FILING DATE: 2006-03-14
PRIOR FILING DATE: 2006-03-14
PRIOR FILING DATE: 1997-03-14
NUMBER: OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.9%; Score 460; LB 12; Length 13); 98.9%; Pred. No. 7.8e-45; tive 0; Mismatches ); Indels
                                                                                                                                                                                                                                                                                                          Length 1919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PSNREETQQKSNLELLRISHLIH | 111.
                PRIOR APPLICATION NUMBER: 07(675,204 PRIOR FILING DATE: 1502-54-27 PRIOR PRILING DATE: 1502-54-27 PRIOR PRILING DATE: 1502-54-27 PRIOR FILING DATE: 1680-16-25 PRIOR FILING DATE: 1980-10-25 NUMBER OF SEQ ID NOS: 20 SEQ ID NOS: 20
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    PRIOR FILING DATE: 1992-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                               90; Conservative
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90; Conservative
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                                                                                                                                                                                                                        IYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-400-377-1
                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                        LENGTH: 191
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US-10-400-708-1
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Best Local S
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98.9%; Pred. No. 9e-45;
tive 0; Mismatches 7; Indels (
PUDICATION NO. US20030153207
FUDICATION NO. US2003015300341
GENERAL INFORMATION:
APPLICANT: Brian C. Cunningham
TILLE OF INVENTION: GROWTH HORMONE VARIANTS
FILLE REPERENCE: 669.12 US-7
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT APPLICATION NUMBER: US/10/153,207
FRIOR APPLICATION NUMBER: 08/499,884
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1994-02-02
PRIOR PILING DATE: 1994-02-02
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/86,066
PRIOR FILING DATE: 1992-04-27
PRIOR FILING DATE: 1989-10-26
PRIOR FILING DATE: 1989-10-26
PRIOR FILING DATE: 1989-10-26
PRIOR FILING DATE: 1988-10-28
NUMBER: OF SEO ID NOS: 20
SUMMER: PASSICATION NUMBER: 07/264,611
PRIOR FILING DATE: 1988-10-28
NUMBER: PASSICATION NUMBER: 07/264,611
PRIOR FILING DATE: 1988-10-28
NUMBER: PASSICATION NUMBER: 07/264,611
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115 PSNREETQQKSNLFLLRISLLLTQSWLEPVQ 145
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US-09-853-688-2
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US-09-280-050-66

I Sequence 66. Application US/09286030A

Sequence 66. Application US/09286030A

Patch. No. 382601002155A1

GENERAL INFORMATION:
APPLICANT: Sato, Seiji
APPLICANT: Koddo, Masaaki
APPLICANT: Wordo, Masaaki
APPLICANT: Koddo, Masaaki
APPLICANT: Wordo, APPANTIBE.
APPANTIBE: PRT
APPLICANT: Wordo, Wordo, Wordo, Wordo, Wordo, Masaaki
APPANTIBE: Wordo, Wordo
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L17:[111:1111.1111...]
27 PPIIPLSKLFUNAMIRAHRLHQLAFOTYQEFESAY:PREGKYSFLQNFGTSLFSSSTIT =)
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                                                                                                             APPLICANT: Cherrykh, Svit.ana I.
APPLICANT: Cherrykh, Svit.ana I.
APPLICANT: Cherrykh, Svit.ana I.
APPLICANT: Cherrykh, Svit.ana I.
APPLICANT: Slavelenko, Iryna YG.
APPLICANT: Slavelenko, Oleksandr
ITI.E OF INVENTION: PRAGE-DEFENDENT SUBER PRODUCTION OF
ITILE OF INVENTION: BACCOCCALLY ACTIVE PROTEIN AND PEPTICES
CURRENT APPLICATION NUMBER: US/09/929.318
PRIOR APPLICATION NUMBER: US/09/318,288
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
NUMBER: OS SEQ ID NOS: 11
SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 460; DB 9; Length 217:
98.9%; Pred. No. 9.26-45;
ative 0; Mismatches 1: Enders
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Sequence 9, Application US/09029918 Patent No. US2002090678A1 GENERAL INFORMATION:
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Best Local Similarity 98.99
Matches 90, Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 90; Conservat
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RENGLY 1:

US-948-748C-4

Sequence 4, Application US/39969748C

Sequence 4, Application US/39969748C

Sequence 4, Application US/3091616591

SEPTICANT NO. 1002001616591

SEPTICANT APLICANT PROBATION.

APPLICANT HOWSTON. 1301. L.

APPLICANT HOWSTON. SERVER

APPLICANT GLAPPN. SERVER

APPLICANTON GLAPPN. SERVER

ATITLE OF INVENTION. COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BLOCCICALLY A

TITLE OF INVENTION GLAPPN. SERVER

FRICK FILING DATE: 2002-12-10

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2000-11-14

SERVEN SEQ ID NOS: 115

SOFTWARE: PATENTIN VERSION 3.0

SSOFTWARE: PATENTIN VERSION 3.0

SSOFTWARE: PATENTIN VERSION 3.0

SSOFTWARE: PATENTIN VERSION 3.0
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Statent No. US20020081665A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: COOPER, DAVID N.
APPLICANT: PROCEER, ANNIE M.
APPLICANT: PROCEER, ANNIE M.
APPLICANT: MILLAR, DAVID S.
ITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN ITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
FILE REPERENCE: WCR78
GURRENT FILING DATE: 201-05-14
NUMBER OF SEQ ID NOS: 66
SSCTWARE PARENTIN Ver. 2.1
SSCTWARE PARENTIN Ver. 2.1
SSCTU NO. 2
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97.8%; Pred. No. 4.5e-44;
tive 0; Mismatches 2; Indels
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Pred. No. 4.5e-44;
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Rest Local Similarity 97.88
Matches 89; Conservative
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CRGANISM: Homo sapiens
US: 09:853-688-2
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; OKGANISM: Homo sapiens
US-09-969-748C-4
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Best Local Similarity
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Mismatches

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89; Conservative

Matches

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Sequence 12, Application US/09824260
Sequence 12, Application US/09824260
Sequence 12, Application US/09824260
Sequence 12, Application OS2030167831A1
SECURALIINO NO. US203030167831A1
APPLICANT: KUSSEML DOUGLAS A.
APPLICANT: SCHLITTLES, MICHAEL
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF BIOACTIVE, ACTHENTIC
TILLE OF INVENTION: EXPRESSION AND PLANTS
FILE REPERENCE: 16712.0031
CCRRENT FPLICATION NUMBER: US/09/824,200
CCRRENT FILING DATE: 2001.04.03
PRICE FILING DATE: 2001.04.03
PRICE FILING DATE: 2001.04.03
PRICE FILING DATE: 2000.04.43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FPTIPLSRLFDNAMLRAHRIHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GORGORE, GINA
TITLE OF INVENTION: THYROID AND PITUTARY MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESONEDNCE ADDRESS: 4
STREEL: 3174 POPPER DRIVE
CITY: PALO ANTO
STATE: CALLFORNIA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                       87 PSNRSETQOKSNLELLRISHLINGSWLEPVQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/850,897
FILING DATE: C7-May-2001
CLASSIFICATION: <UNKNOWN>
PRICE APPLICATION DATA:
PSNREETCOKSNLELLRISHLIOSWLEPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/087,678 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application CS/09850887; Patent No. US20020009778A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CERRONE, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
CCMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentl: Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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LENGTH: 191
TYPE: PRI
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                  2 FPT:PLSREFONAMIRAHRLHQLAFDIYQEFFEAVIPKHGKYSFLGNPGTSESHSTFT A.
                                         7: FPITELSKEFDNASLAHREGGLAFOTVOEFEBAYTPKECKYSFJONFOTSLAFSETT 86
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APPLICANT: PROCTES, ANNIE M.
APPLICANT: PROCTES, ANNIE M.
APPLICANT: MILLAR, DGEN
APPLICANT: MILLAR, DGEN
TITLE OF INVENTION: METHOD FOR DEDCTING GROWTH HORMONE VARIATIONS IN
TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THERR USES
FILE REPERSINCE: WORTH
                                                                                                                                                                                                                                   US-69-804-409a-16
Sequence 16. Application US/09864469A
Patent No. US/020155196A1
GENERAL INFORMATION:
APPLICANT: KIEFFER, TIMOTHY J.
APPLICANT: CHEUNG, ANTHONY T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
TITLE OF INVENTION: EXPERSSION IN GUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%; Score 453; DB 10; Length 217; 97.9%; Pred. No. 5.8e-44;
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96.78; Pred. No. 2.8e-43;
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                                                                                                      62 PSNPEETQQXKSNLPIGGRISGGGGSWLEPVQ 92
11 (111 - 1115 - 111 - 111 - 111 - 111
82 PSNREETQQKSNLEGERISGGLIGSWGEPVQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NOWBER: 05/09/864,409A
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEC 13 NOS: 18
SOFTWARE: Patentin Ver: 2.1
SEC 1D NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: JS/09/851,688
CURRENT FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATCHILD VS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4. Application US/09853688 Patent No. US20026081605A1 GENERAL INFORMATION:
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Best Local Similarity 96.79
Watches 88: Conservative
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Matches 89; Conservative
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US-09-853-688-4
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Best Local Similarity 84.5%, Prod. No. 1.9e-37,
Matches 77; Conservative 6; Mismatches 8; Indels
REFERENCE/DOCKET NOMBER: PF-0535 US
FELDENOWICNET CATION INFORMATION:
FELDENOWIS: (650) 855-055
FELDENAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERIS:
FYPE: amino acid
STRANDENESS: Single
TYPE: amino acid
STRANDENESS: Single
TOFOLGY: Innear
INMEDIATE SOURCE:
LIBBARY: GenBark
CLONE: 4606987
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-69-850-867-3
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Search completed: September 15, 2003, 12:23:35 Job time : 38:5806 secs

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Copyright (c) 1993 - 2003 Compagen Ltd.
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- protein search, using sw model OM protein 5 ; Search time 15.1685 seconds (Without alignments) 583.284 Killion cell updates/sec 2033, 11:56:45 September 15, Run on:

US-03-423-100-2

Title:

NUMBERSHIELLGSWIEDVL 470 1 MEPTIPLSRLEDNAMLRAHK.. Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

38330H Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 3%

PIR_76:*

1: piri:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	CB		Description
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7	460		217	2	167410	
٣:	422	60 (T)	217	_	STRUV	C4
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9	397		217	~	167409	ar Es
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œ	336		217	e4	153267	
(ħ	381		217	.⊣	LCHUC	cherionammetrepin
10	381		217	:7	E32435	choriomammotropin
11	359.5		215	(7	A26449	cheriomeanmotrepia
12	310.5		216	(1	B49159	Somate: ropin - del
13	307.5		190	13	PN0140	'
14	304.5		216		STMS	Ċ.
15	302.5		190	7	STHC	
16	302.5	54.4	216	٦	SIRT	
17	302.5		216	٤٧	549483	
an c t	301.5		190	C4	JK5219	
19	301.5		215		8150	somatofropin procu
20	301.5		216	7	146145	scratotropin precu
21	301.5	6.1	216	?	JC4632	
22	299.5	. 9	216	£4	A37782	sonatotropin precu
23	297.5	63	061	٠,	A51584	
24	295.5	6.2	0007	~	JS0429	
25	289.5	9	217	·	STBC	Somato: robin precu
26	289.5	61.6	217	, .	STSH	Sometatropin prequ
27			217		SIGT	sematetropin preeu
28	289.5	66	217	7	S32582	somatotroton dom
29		S)	216	7	JC1514	Ξ.

A.Kolecule type: mRNA
A.Kesiques: 1-217 <MARA
A.Kesiques: 1-217 <MARA
A.Kesiques: 1-217 <MARA
A.Kesiques: 1-217 <MARA
A.C. Siochem. Biophys. 133, 70-11, 1969
A.Title: Human pituicary growth hormone. XIX. The primary structure of the hormone
A.Kedference number: A50648; MJID:69289202; PMID:5810834
A.Contours: annotation
B.Li. C.H.: Dixos, J.S.
Atch. Biochem. Biophys. 146, 233-236, 1971
A.Title: Human pituitary growth hormone. XXXII. The primary structure of the hormon A.Reference number: A90651; MUID:72143935; PMID:5144027

A: Molecule type: protein A; Accession: A90051

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A60509	A60625	504929	S21750	A55816	151188	350037	B32435	151256	A60623	167761	JTC483	CNC387	CC5682	153763	538353
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	268.5 57.1													165.5 35	

ALIGNMENTS

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Species: Homo sapiens (man) preprints, summarylippin 1, long form; somatotropin 1, chate: 24-Apr-1984 #sequence_revision 10-Feb-1995 #text_change 08-Dec-2000 CiAccession: A93731. A32435, A93649, A94247; A90051; A93397; A93778; A91764; A9621 A1Deric Acids Res. 9, 3719-3730, 1981 A1Titie: Human growth hormone DNA sequence and mRNA structure: possible alternative A:Reference number: A93731; MUID:82014939; PMID:6269091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Accession: A32435
A.Molecule type: DNA
A.Rosious: 1-217 CHE>
A.Coross-references: GB:J03071; NID:g183148; PIDN:AAA52549.1; PID:g183149
A.Coross-reference number: A93694; MUID:80034477; PMID:386281
A.Accession: A93694
A.Accession: A93694
A.Rosioucs: 1-217 CROS
A.Coross-references: GB:V06519
A.Coross-ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Wolecule type: DNA
A:Cross-1-217 <DEN>
A:Cross-references: GB:V00520
A:Note: the 20K short (5rm somatotropin lacks residues 58-72 (32-45 in the active
Genomics 4, 479-497, 1989
A:Title: The human growth hormone locus: nucleotide sequence, biology, and evoluti
A:Reference number: A32435; MUID:89307277; PMID:2744760
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A.Tille: Haman growth hormone: complementary DNA cloning and expression in bacteri A.Reference number: A94247; MUID:79203293; PMID:377496
somatotropin ; precursor [validated] - human
N.Alternate names: growth hormone 1; EGH-N; pituitary somatotropin
N.Contains: growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1,
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of

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Cibale: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
CiAcrossion: 164410, A0530,
Endocrinology 1.3. Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A/TILL: Choining of Four growth hormone/chorionic somatomanmolropin-related complem A:Relevence number: 153267; MUTD:94008724; PMID:8404617
                                   Comment: The gene for this hormone is transcribed only in somatctrophic cells Comment: About 90% of somatotropin is the 22K long form. Commenters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                 A.Cross-references: GDB:119982, OXIM:139250
A:Map position: 17q23.1-17q23.3
A.Introns: 4/1; 57/3; 97/3; 152/3
E.1-26/Doxaln: signal sequence *status predicted <SIG>E.1-26/Doxaln: signal sequence *status predicted <SIG>E:27-69/Product: somatotropin 1, long form *status experimental <SOS>E:27-69/Product: somatotropin 1, short form *status experimental <SOS>E:27-57,73-217/Product: somatotropin 1, short form *status experimental <SOS>E:27-57,73-215/Disulfide bonds: *status experimental
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A:Contents: annotation; identification of source organism
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Astatus: translated from GH/EMBL/DDBJ
Astatus: translated from GH/EMBL/DDBJ
Astatus: translated mRNA
Astatus: 1-217 cRES>
Astatus: 1-217 cRES>
Astatus: 1-217 cRES>
Astatus: Gist Chung, D.: Lahm, H.W. Stain, S
Asti, Cist Chung, D.: Lahm, H.W. Stain, S
Asti, Leit Chung, D.: Lahm, H.W. Stain, S
Asti, Leit Chung, Structure of monkey pituitary growth hormone.
Astatemence number: A05094; MUID:86129466; PMID:3080959
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Best Local Similarity 98.9%; Pred. No. 4.4e-42;
Matches 90; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 460; DB 1;
Pred. No. 4.4e-42;
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A:Residues: 27-99, 'Q',101-178,'D',180-217 <LIC>
A:Note: the monkey species is not identified in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Species: Macada mulatta (rhesus madaque)
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N:Alternate names: growth hormone
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Best Local Similarity 98.9°
Matches 90; Conservative
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                                                                                                                                                                 A,Gene: SDB:GHI
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R. Messidues: 17-94-16-217 - 1220-
R. Messidues: 17-94-16-217 - 1220-
R. Malline for State: 140, 60-214.
Million for Milli
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Chacession: [674]]
Bidolos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.
Bidolos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.
Bidolosy, 133, 1744-1752, 1993
ASSILLE: Cloning of four growth hormone/chorionic somatomanumolropin-related complemance number: 153267; MJID:94008724; PMID:8404617
                                                                                                                                                                                                                                                                                                                              Clacession: Asserts as equecies is the control of the last acceptance of sep 1997 (Clacession: ASD) and the control of the con
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C:Spocies: Macaca mulatta (rhesus macaque)
C:Cate: 31:May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                 C:Species: Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 10-Feb-1995 #text_change 02-Sep-1997
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AJGTOSS-roferoncos: GB:L16555; NID:g293116; PIDN:AAA20180.1; PTD:g293117
G/Superfamily: prolactin
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A.Sect. 508:642
A.Sect. 508:642
A.Sect. 508:642
A.Map position: 17422-17424
A.Map position: 17422-17424
A.Map position: 17422-17424
C.Suportarily: prolactin
C.Suportarily: prolactin
C.Seywords: alternative splicing; hormone; placenta
F.1-26/Pomali: signal sequence status predicted <SIG-
F.26/Product: somatotropin 2 splice form 2 *status predicted <MAT>
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A:Note: an alternative splice junction for introm 4 is used
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Pred, No. 6.7e-36;
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A, Status: preliminary: translated from GB/EMBL/DDHJ
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                                                                                                                         somatotropin 2 precursor, splice form 2 - human
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1 Similarity 92.3%;
84; Conservative
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Best Local Similarity 85.77
Matches 78, Conservative
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Best Local Similarity
Matches 84; Consery
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A; Molecule type: mRNA
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somatotropin 2 precursor - human
Nationate names growth hormone 2; growth hormone variant, 58H-V; placental sumutified
N/Alternate names growth hormone 2; growth hormone variant, 58H-V; placental sumutified
C/Species: Homo sapiens (man)
C/Species: A 479-492, 1889
A/Hitle: The human growth hormone locus: mucrocide sequence, biology, and evolution:
A/Reference number: A32435, MUID:89307277; PMID:244766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Molecule type: DNA
A)Residues: 1-217 <0HE.
A)CCOKE, N.E.: REW, G.: BEADSOTE HID:G183146: PIDNEAAA52552.1; Filteries(55)
B)CCOKE, N.E.: RAY, G.: Bmery, d.G.: Liebhaber, S.A.
J. Bloi. Chem. 263, 9001-9906, 1986
J. Bloi. Chem. 263, 9001-9906, 1986
A)Title: Two district, species of buman growth hormone-variant manh in the buman personal
A)Reference number: A92725: MUID:88243769; PMID:879657
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A. Residues: 1-217 <COO-
R. Sesidues: 1-34 '9' 1982
A. Title: The human growth hormone gene tamily: nucleotide sequences show recent diverged A. Accession: A015: 1
A. Molecule type: ON R. L. Frankenne, F.; Hennen, G.
A. Molecule type: Diaching and nucleotide sequence of placental high-V chka.
A. Reference number: 152104; MUID: 89624984; PMID: 2460360
A. Title: Cioning and nucleotide sequence of placental high-V chka.
A. Reference number: 152104; MUID: 89624984; PMID: 2460360
A. Status: proliminary: translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Residues: 1-217 <coo-
A. Gross references: GB: MB451; MD: 91317018; PMID: 2196276
A. Reference number: A60711; MJD: 90317018; PMID: 2196276
A. Molecule type: protein
A. Residues: 27-44,46-57 <coor
A. Residues: 27-44,46-57 <coor
A. Resperimental source: tissue placental
A. Roto: partial source: tissue placenta
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A.Introns: 4/1: 57/3: 97/3: 152/3
A.Introns: 4/1: 57/3: 97/3: 152/3
A.Introns: 4/1: 57/3: 97/3: 152/3
A.Introns: 4/1: 57/3: 97/3: 97/3: 152/3
A.Introns: 4/1: 57/3: 97/3: 97/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 152/3: 15
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Pred. No. 5.50-38:
3: Mismatches 4: Indels
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1 Similarity 92.3%;
84; Conservative
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A:Gene: GDB:GH2
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Best Local S
Matches 84
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C. Species: Howo sapiens man and continue constants are continued to the constants in the constants in the constants in the constants in the constant in the c
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A)Reference number: A94427

A)Accession: A94427
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                                                                                                                                                                                 3 PTIPLSRLFDNAMLRAHRLHQLAFJTYQEFEBAYIPKSOKYSFLONPQTSLSFSESIPTP 62
                                                                                                                                                                                                                    choriomammotropin A precursor [validated] - human
N:Alternate names: chorionic somatomammotropin 1; placental lactogen
                                                                                                                    ö
                                                 Length 217;
                                                                                                                 Indeis
                                              84.3%; Score 395; DB 2; I
82.2%; Pred. No. 3.4e-35;
ive 11; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                       63 SNREFTQQKSNLELLRISLLLIQSWLEPVQ 92
              Sust Local Similarity 82.2% Sust Local Similarity 62.2% - A. Conservative
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Cispecies: Macaca mulatia (rhesus macaque)
Cispate: 31 may 1996 #sequence_revision 31-may-1996 #text_change 16.311-1999
Ciscession: 153267
Rigolos, T.G.: Durning, M.; Fisher, J.M.; Fewler, P.D.
Endocrinology 133, 1744-1752, 1993
Affile: Cloning of four growth hormone/chorionic somatomammetropin-related complemental
A;Reference number: 153267; MulD:94008724; PMID:8454617
A;Accession: 153267
A;Accession: 153267
A;Accession: 15327
A;Melecule type: mRNA
A;Nesidues: 1-217 <RES>
A;Cross:references: GB:L16552; NID:9293108: PIDN:AAN18839.1; PID:g253:09
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167408

Lobolook somatomammotropic-2 - ricsus macaque (fragment)

C; Species: Macaca mulatta (rhesus macaque)

C; Species: Macaca mulatta (rhesus macaque)

C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1939

C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1939

R; Golos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.

Brdoctinology 133, 1744-1752, 1993

A; Title: Cloning of four growth hormone/chorionic somatemmamorropin-related rempiamment in 15/408

A; Reference number: 153267; MUID:9408724; PMID:8404517

A; Reference 153267; MUID:9408724; PMID:8404517

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residuale type: mRNA

A; Cross-references: GB:L16553; MID:9293110; PIDN:AAA18846.1; PID:m28411;

C; Superfamily: prolactin
C:Species: Macaca mulatia (rhesis manague)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #lext_change letin1-1999
C:Cossion: 16740
B:Golos, T.G.: Durning, M.; Fisher, J.M.; Fowler, B.D.
Endocrinology 133, 1744-1752, 1993
A:Title: Cloning of four growth hormone/chorionic somatomammolicopin-rolated complementar A.Reference number: 153267; MUID:94003724; PMID:8464617
A.Reference number: 153267; MUID:94003724; PMID:8464617
A.Residue: preliminary; translated from 3B/EMBL/2003J
A.Residues: 1-217 <-RES>
A.Cross-references: GB:L16554; NID:g293112; PIDN:AAA:8941.L: PID:g29313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.5%: Score 397; DB 2; Longth 217;
illarity 83.3%; Pred. No. 2.7e-35;
Conservative 8; Mismatches 7; Indels
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Matches 74; Conservative
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Best Local Similarity
Thes 75, Conserva
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us-09-423-100-2.rpr

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D.H.; Harrera-Saldana, H.A.; Gelinas, R.E.; Seebur
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                                                                                                                                                                                                                                                    biology, and evolution
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Endocrinology 129, 2465-297; 1991
A.Title: Sequence and expression of hamster prolactin and growth hormone messenger
A.Reference number: A49159; MulD:92063850; PMID:1954881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Accession: A26449
R:Hirt, H.; Kimelman, J.; Birnbaum, M.J.; Chen, E.Y.; Seeburg, P.H.; Eberhardt,
DNA 6, 59-70, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                          C.Species: Homo sapiens (man)
C.Date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NALTernate names: growth hormone
Cisperies: Mesocricetus auratus (golden hamster)
Cipace: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jui-2000
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C:Date: 30-Jun-1988 #sequencc_revision 30-Jun-1998 #text_change 28-Jul-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: GB:JC3071: NID:g183148; PIDN:AAA52553.1; PID:g183153
CGenetics: GFB:
A:Genetics: GFB:SH2
A:Gross-references: GDB:119813; OMIM:118820
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C:Superfamily: production
F:51-26/Domain: Signal Sequence #status predicted <SiG>
F:27-215/Product: choriogammotropin, hCS-3 ailele #status predicted
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                                                                                                             Clacession: E32435
Richer, E.Y.; Lido, Y.C.; Smith, D.H.; Harrera-Saldana, H.A.; Genomics 4, 479-497, 2899
Alithe: The human growth hormone locus: nucleotide sequence, I Azeteronce number: A32435; MJID:89307277; PMID:274476
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R0.5%; Pred; No. 2.9e-31;
. Vismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 381; DB 2; 1
Pred. No. 1.4e-33;
8; Mismatches 8;
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        NiAlternate names: chorionic somatomammotropin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 NREETQOKSNLELLRISLLLIQSWLEPVQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NREETQQKSNLELLRISLLLIQSWLEP 90
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G:Superfamily: prolactin
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Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary
A:Wolecule type: DNA
A:Residues: 1-217 <CHE>
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                         Afresidios: 27-217 ck. A. A. Residios: 27-217 ck. A. A. Residios: 27-217 ck. A. A. Residios: 27-217 ck. A. A. A. Barchamental source placenta R. B. Experimental source placenta R. B. Experimental source placental R. B. A. Tipton, K. F. Biochem. Soc. Trans. 19, 26s, 1991
A. A. Miller: Catechol-Ornechlyltransferase from human placental purification and some property A. A. Reference number: A61283 kMUD1912440366; PMTD12637148
A. Residues: 27-46 ck. IC.
A. Modecule type; protein
A. Residues: 27-46 ck. IC.
A. Modecule type; protein
A. Residues: 27-46 ck. IC.
A. Modecule type; protein
B. Sherwood, L. M.: Handwerger: S.; McLaurin, W. B.; Lander: M.
A. Title: Anino-acid sequence to Human placental taveogen.
A. Reference number: A93405
A. Title: Anino-acid sequence to Human placental taveogen.
A. Reference number: A93405
A. Reference number: A93251; MCID: A11140; MCID: Experiment M.
B. Scherwood, L. M.; Bardar A. Bartar A. Bartar
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Astatus: translated from GB/EMBL/DDBU
Astatus: translated from GB/EMBL/DDBU
Astatus: translated bun
Astatus: Lainslated from GB/EMBL/DDBU
Astatus: translated bun
Astatus: Masoco, Am. Physicians 90: 109-116, 1977
Artitle: Nucleotide sequence of a human gene noding for a polypeptide hormone.
Astatus: Laraslated from GB/EMBL/DDBU
Astatus: Laraslated from GB/EMBL/DBU
Astatus: Carross references: GB-INGBU
Astatus: Astatus experimental (Carross from Status experimental Estatus Estatus Estatus Estatus Estatus Estatus
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E32435
chorlomammotropin B precursor - human
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hes 73, Conservative
A;Molecule type: protein
A;Residues: 27-217 <NIA>
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Matches

g 8 Length 216;

DB 1:

14; Mismatches 17; Indels

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2 FPTIPLSKLFUNAMLKAHKLHOLAFDTYOEFEEAYIPKEQKYSFLONPOTSLSFSESIPT 61
                                                                                           64.8%; Score 304.5; DB 1
64.8%; Pred. No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 15, 2003, 12:04:19 Job time : 16.1685 secs
                                                                                                    Query Match
Best Local Similarity 64.8%
Matches 59: Conservative
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CiSpecies: Mus musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiSpecies: D.I.H.: Talamantes, F.
J. Biol. Chem. 260, 9574-9579, 1985
A:Title: Nuclectide sequence of mouse projectin and growth hormone maxas and expression
A:Reference number: A92548; MUID:85261358; PMID:2951252
A:Accession: B2391
A:Accession: B2391
A:Accession: B2391
A:Residues: 1-216 <LINA
A:Residues: 1-216 <LINA
A:Residues: 1-216 <LINA
A:Residues: anterior pituitary; growth factor; hormone
C:Superfamily: projection
C:Superfamily: projection
C:Superfamily: signal sequence status predicted <SIG>
F:78-186/Droduct: somatotropin #status predicted
F:78-189,206-214/Fisulfide bonds: #status predicted
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C. Species: Balaecoptora borealis (sei whale)

C. Species: Balaecoptora borealis (sei whale)

C. Species: Balaecoptora borealis (sei whale)

C. Sacession: PNO. A. Set whaten the set of th
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A,Accession: B49159
A;Status: preliminary
A;Status: preliminary
A;Status: 1-216 <SGU>
A;Cross-references: GB.SG6299; NID:q239355; PIDN:AAB326468.11; PID:q239346
A;Cross-references: GB.SG6299; NID:q239355; PIDN:AAB326468.11; PID:q239346
A;Note: sequence extracted from NCB: packbone (NCBIN:66299; NCBID:G6376)
C;Supcrfamily: prolaction
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Pred. No. 5.5e-26;
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C:Superfamily: productin
C:Keywords: growth factor: hornone
F:52-i63,180-188/Disulfide bonds: *status predicted
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67.08;
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Attacession: A918-13

Attacession: A902-14

Attacession: A902-14

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                                                                                                                                                                                                                                                                                                                                                                      NAlternate names: growth hormone
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Accession: 13-Jul-1981 4sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C;Accession: 1491772; 491395; A01383; A01340; A01514
R;Zakin, M.M.; Poskus, E.: Langton, A.A.; Ferrara, P.; Santome, J.A.; Dellacha, J.M.
Int. J. Pept. Protein Res. 8, 435-444, 1976
A;Titlo: Primary structure of equinc growth hormone.
A;Ricorence number: A01772.
A;Accession: A91772.
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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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A/Residues: 176-190 <cL1>
C/Superfamily: projection
C/Superfamily: projection
F/52-163/190-188/Disulfide bonds: *status experimental
                                                                                                                                 62 PSNREETQQKSNLELLRISLLIJQSWLEPVQ 92
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Host Local Similarity 64.88
Matches 59, Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2003, (1:04:00 : Sequencial connects)
(without alcohorus)
504.63) Million cell updates/see Run on:

US-00-423-100-5

DARIEMSCHIEUSERITERING 1 MEPTIPLSRLFDNAMLRAHR. Title: Perfect score: Sequence:

BLOSUM62 Gapop 16.0 / Sapext 6.5 Scoring table:

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2600656(60

Post-processing: Minimum Match 160% Maximum Match 160% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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SUMA_CRONO	SOMA_CHEMY	SOMA_ANAPI.	SCM1_ACIGU	SOM2_ACIGU	SOMA_LEPOS	SOMA_XENLA	SOMA_RANCA	SOMA_BUFMA	SOMA_PRIGL	SOMB_XENLA	SOMA_PROAN
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58.0	57.1	55.5	54.8	54.8	52.7	51.0	50.7	48.2	48.0	45.7	46.5
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AL IGNMENTS

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SCMA_HUMAN STANDARD: PRT: 217 AA.
P01241: 014405; C16631: 09HS21: 09UMJ7: 09UMJ7: 09UMJ5: 21-401:-1986 (Rel. 01. Created)
01-MAR-1982 (Rel. 21. Last: accence update)
15-5RF-2063 (Rel. 42. Last: amontation update)
Scmatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. ("SOFORM 1).
MEDIJNEPAD203232; Pribmed-377486; Martisl J.A., Halleweil R.A., Baxter J.D., Goodman H.M.; Martisl J.A., Halleweil R.A., Baxter J.D., Goodman H.M.; "Human growth hormone: complementary DNA closing and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89307277; FibMed 2744769; Chem E.Y., Siao Y.C., Smith D.H., Barrera-Saldana H.A., Galhas R.E., Seebury P.H.; The human growth hormone locus: nucleotide sequence, biology, and methods for ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND POSSIBLE ALTERNATIVE SPLICING. MEDLINE-82014939; Pubmed-6269091; Denote P.M., Moore D.D., Goodman H.M.; "Human growth bronce D.D., Goodman H.M.; alternative splitting.":

**Alternative splitting.":
Nucleic Acids Res. 9:3719-3730(1981).
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"The Luman growth hormone gene family: nucleotide sequences
recent divergence and predict a new polypeptide hormone.";
DNA 1:239-249(1982).
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Eukaryota: Metazoa; Chordata: Craniata: Vertebrata: Eutele
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
NCBI.TaxID=9606;
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MEDLINE-80034477; PubMed-386281;
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                                                                                                                                                                                                                                                                                              Germone) (Growth hormone 1).
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Gray G.L., Baldridge J.S., McKeown K.S., Reyneker H.L., Chang C.N.; "Periplasmic production of correctly processed human growth hommone in Escherichia coll: natural and bacterial signal sequences are interchangeable."; Gene 39:247-254(1985).
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MEDLINE-7153968: PubMed-5279528;
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"Sequences of pituitary and placental lactogenic and growth hormnes:
evolution from a primorbal poptide by dene reduplication.";
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Li C.H., Dixon J.S., Liu W.-K.;
"Human pituitary growth hormone. XIX. The primary structure of
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Bewiey T.A., Dixon J.S., Li C.H.;
"Sequence comparison of human pitulitary growth hormone.
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Nature New Biol. 230:90-91(1971).
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"The chemistry of the human lactogenic horrones.";
(In) Griffiths K. (eds.);
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                                     TISSUE-Pituitary;
MEDLINE-20402571; PubMed-19931946;
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MEDLINE=86137393; PubMed#3912261;
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MEDLINE-80130196; Pubmed=7356479;
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IN C.H., Dixon J.S.:
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MEDLINE-71139765; PubMed-5279046;
                   FROM N.A. (ISOFORM 4).
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MEDLINE-95075462; PubMed-7984244;
Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
"The X-ray structure of a growth hormone-prolactin receptor complex.";
Nature 372:478-481(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- FUNCTION: Plays an important role in growth control. Its major role in stimulate that ing body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates
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icewis U.d., Bonewald L.F., Lewis L.J.;
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                                                                                                      2 PPTIPLSKLFDNAMIRAHRIHQIAFUTYQBFERAYIPKBOKYSFIGNPOTSLSPSFS1PT 61
                                                                                                                                              27 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQSFFHAYTPKHQKYSFLUNGUSTOFSFSTFF 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94009724: PubMed-1404617; Golos T.G., Durning M., Pisher J.M., Fowler P.D.; Golos T.G., Durning M., Pisher J.M., Fowler P.D.; Conjug of four growth hormone/Choritonic somatomamotropin-related complementary deoxythonoutleic acids differentially expressed during pregnancy in the rhesus mankey placenta."; Endocrinology 133:1744-1752(1993).
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Mammalia, Butheria, Primales: Catarriles: Geroopithecidae,
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             Score 460: 78 1; Length 217:
Pred. No. 8.6e 41;
Mismatches 1: Indels
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E -> Q (IN REF. 2),
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01-601-1994 (Rel. 30, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                 Score 460;
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                                     Best Local Similarity 98.9
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revol A. Esquivel D., Santiago D., Barrera-Saldana H.:
"Independent duplication of the growth hormone gene in three
Anthropoidean lineages.";
Submitted (APR-2201) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays an important role in growth control. Its major
role in stimulating body growth is to stimulate both: the
other tissues to secrete IGF-1. It stimulates both: the
differentiation and proliferation of myoblasts. It also stimulates
amino acid uptake and proliferation synthesis in muscle and other
tissues (By similarity).
-!- SUBCELDULAR JOCATION: Secreted.
-!- SUBCELDULAR JOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE SOMAIOTROPIN/PROLACTIN FAMILY.
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28-FEB-2005 (Re), 41, Last annotation update)
Somatciropin precursor (Growth hormone) (GH) (GH-N) (Pitultary growth
                                                                                                                                                                                      2 FPTIPLSRLFUNAMLKAHKLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa: Chorduta, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butherla, Primates, Catarrhini, Hominidae, Pan.
NCBL_TaxID-9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                  0:
                                                                             Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
N -> D (IN REF. 2).
2C5180341REC46D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEA295EDE0518674 CRC64;
                           Score 450; DB 1; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 1;
8.8e-41;
                                                                                                                                                                                                                                                                                                                   62 PSNREETÇQKSNLELLRISELLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AA
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BY SIMILARITY.
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                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 460;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0836 SOMATOTROPIN.
PROSITE: PSO0266: SOMATOTROPIN.1: 1.
PROSITE; PSO036: SOMATOTROPIN.2: 1.
PROSITE; PSO038: SOMATOTROPIN.2: 1.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001460; Somatotropin.
Pfam; PF00163; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-FEB-2003 (Rel. 41, Created)
                      24913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF374232; AAL72284.1;
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                                                                             94.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normone) (Growth hormone 1).
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                                                                                                         98.98;
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Best Local Similarity 96.99
Marches 90, Conservative
                                                                                                                                     Conservative
1/9 1
217 AA;
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                                                                                                   Local Similarity
nes 90, conserv
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NCBI_TaxID=9598;
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P58757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SCOOR REPRESENTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a nollaboration between the Swiss Institute of Bioinformatics and the EMEL Oritstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See Mitp://www.isbraib.ib/announces/or send an email to license*isbraib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saimiri boliviensis boliviensis (Bolivian squirrel monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatas; Platyrrhini; Cebidao; Cebinae; Saimiri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissees (By similarity).
SUBCELLULAR LOCATION: Secreted.
SIRILARITY: BELCNGS TO THE SOMATOTROPIN/PROLABITIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Longth 217;
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HY SIMILARITY.
BY SIMILARITY.
1 951526992052097 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.1%; Score 433: DB 1:
91.2%; Pred, No. 5.60-48;
                                                                                                                                                                                   28-FEB-2003 (Rel. 4], Created)
28-FEB-2003 (Rel. 4], Last sequence update)
28-FEB-2003 (Rel. 4], Last annotation update)
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               PSNREETOOKSNLELLRISLLLIQSWLHPVO 92
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                                                                                                                                                                                                                                             Somatotropin precursor (Growth hormone)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00266; SCMATOTROPIN_3: 1. PROSITE: PS00338; SCMATOTROPIN_3: 3.
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AF339060, AAK62287.1: -.
INTREPRO: PROJUGO: SOMBIOLINGELE.
PFOLOS: Kormone: ..
PRINTS: PROGR36: SOMATO: BC 910.
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                                                                                                                                                 STANDARD;
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215
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217 AA:
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                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=39432;
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Q9GMB3;
                                                                                                                                               SOMA_SAIBB
P58343;
               62
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                                                                                                                                                 STATE THE STATE OF ST
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                                                                                                                                                                                                                                                                                                                                                                                                               Wallis O.C., Wallis M.;

"Cloning and characterisation of a putative growth hormone encoding
"cloning and characterisation of a putative growth hormone encoding
"cloning and characterisation of EMBL/GenBark/DDBJ databases."

Submitted (AUG-2000) to the EMBL/GenBark/DDBJ databases.

-! FUNCTION: Plays an important role in growth control. Its major
role in stimulating body growth is to stimulate the liver and
other tissues to secrete IGF-1. It stimulates both the
differentiation and proliferation of myoblasts. It also stimulates
amino acid uptake and protein synthesis in muscle and other
Lissues (By similarity. Secreted.
-: SUBCELLUIAR LOCATION: Secreted.
-: SUBCELLUIAR LOCATION: Secreted.
-: SUMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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                                                                                                                                                                                                           Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes (Chimpanzee).
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 217;
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91.2%; Pred. No. 7.2e-38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E102151A12CE6192 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
26-FBB-2303 (Rel. 41, Created)
28-FBR-2303 (Rel. 41, Last sequence update)
26-FBB-2303 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PSNREETQCKSNLHLLRISLLLSGSWLEPVO 92
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                                                                                                         Somatotropin precursor (Growth hormone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PFO0103; hormone; Dramstotropin.
PROSITE; PS00265; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
SIGNAL
SIGNAL
                                                                                                                                                                              Callithrix jacchus (Common marmoset).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001400; Somatctropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ297563; CAC03481.1: -. HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hormone) (Growth hormone 2).
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nes 83: Conservative
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237 AA;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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proteins.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss lestitude of Bloinformatics and the EXMT outstation the European Bloinformatics Institute. There are no restrictions or its
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformation of Bioinformation and the BME outstatum use by non-profit institutions as long as its content, is in an advantate and file and this statement is not removed. Usage by and this statement is not removed. Usage by and for commencial entities requires a license agreement (See http://www.sb-stb.ch/ancounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PPTIPLSKLFDNAMLRAHRLHQLAFDTYQFFEEAYIPKEQKYSFLONPOTSLSFSESIFT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2001) to the EMBL/Geobank/DDBJ databases.

-!- FUNCTION: Plays an important role in growth control. Its major role in stimulation dony growth is to stimulation. The liver and other tissues to secrete (RF-1, it stimulates both the differentiation and prollieration of myobiasts. It also stimulates amino acid uptake and prollieration of myobiasts. It also stimulates amino acid uptake and prollieration synthesis in miscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01242. P09587.
21-JUL-1966 (Rel. G., Greated)
28-FEB-2003 (Rel. 41, Last Sequence update)
15-SEP-2003 (Rel. 42, Last annobation update)
Growth hormone variant preparesor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Motazoa, Chordada, Craniala, Vertebrata, Enteleostumi)
Mammalia, Eutheria, Primatus, Catarrhin), Rominidae, Hono,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human growth hormone jene family: nucleotide sequences show
                                                                                                                                                                                                                                      tissues.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed in the placency.
SIMILARITY: HELONGS TO THE SOMATOTROPIN/FROLACTIN FAMILY.
                                          Revol A., Esquivel D., Sanniago D., Barrera-Saldana H.; "Independent duplication of the growth hormone gene in three Anthropoidean lineages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recent divergence and predict a new polypeptide hormone.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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BY SIMILARITY.

1592A429075677DE GRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
GROWTH HORMONE VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.5%; Score 430; DB 1; 93.4%; Pred. No. 1.2e-37; ive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 PSHRVKIQCKSNLELLKISLLLICSMLEFVQ 117
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MEDLINE=88243769; PubMed-3379057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00103; normone; 1.
PROSITE; PS00266; SOMATOTROPIN_; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF374233; AAL72285.1; -.
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISCFORM 1).
MEDLINE-83182010; PubMed-7169009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24990 YM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone) (Growth hormone 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 AA;
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Hes 85; Conserv
[1]
SEQUENCE PROM N.A
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208
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linked or non-covalently associated, in homopolymeric and
heteropolymeric combinations. Can also form a complex either with
OHBP or with the aipha2-macroglobulin complex.
SUBCELDULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Suman growth hormone locus: nucleotide sequence, biology, and evolution.";
Cooke N.E., Ray J., Emery J.G., Liebhaber S.A.; "Two distinct species of human growth hormone-variant mRNA in human placenta predict the expression of novel growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId*P01242-2; Sequence*VSP_006203;
Note*no experimental confirmation available;
-!-TISSUE SPECIFICITY: Expressed in the placenta.
-!-SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                           "Cloning and nucleotide sequence of placental hGH-V cDNA."; Arch. Int. Physiol. Biochim. 96:63-67(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-89307277; PubMed-2744760;
Chem E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A.,
Gelinas R.E., Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms=2;
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ISOId=P51242-1; Sequence=Displayed;
Name=2: Syncopyms=3H-V2;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-8924964; Pibmed-2460050;
Tgott A., Scippo N.L., Frankenne F.,
Toloning and nacleotide sequence of p
                                                                                                                                                            Biol. Chem. 263:9001-9006(1988).
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TISSUE-Placenta;
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Best Local 3
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               modified and this statement is not removed. Usage by and for oversorial entities requires a license agreement (See Mitp://www.isb sib.ob/anacurer/or send as email to license@isb-sib.ob).
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RLEDGSPRTGQIFNQSYSKPDTKSHNODALLKNYGLLYGFR
KOMDKVETFLRTVQCRSVEGSGGF -> VHVAPGIPNPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LASRDWGEKHOGPLFSSQALFUENSPYSSFPLVNPPGLSLU
PGGEGGKWANDRGREDGFSAWPLILFLHFAEAGHWQPPDWA
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-203 (Rel. 41, Last, ameriation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosiomi;
Mammalia, Eutheria, Primatos, Catarrhini, Cercopithecidae.
                                                                                                                                                                                                                                                                                                                                                                                           Hormone, Placenta, Signal, Glycoprotein; Alternative splicing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 422; DB 1; Length 217; Pred, No. 7.8e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId-VAR 014591.
I -> T (IN REF. 2).
7B9324698E822F96 GRC64:
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/FIId-vsp_c06293.
R -> w (IN dbsNP:5389).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Mismatches
                                                                                                                                                                                                                                                                                               GO; GO:0005180; F:peptide hormone; TAS
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00103: hormone; 1.
PROSITE; PS00266; SOMATOTRGPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
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                                                                                                                                                                                                                                                                                                                   InterPro: IPR001400: Somatotropin
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                                                                                       EMBL; BC020760; AAH20760.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Conservative
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                                                                                                                                                                                                    PIR; A28072; STHUV2.
PIR; D32435; STHUV.
HSSP; P01241; 1A22.
Genew; HGNC:4262; GH2.
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                  MIM; 139240;
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1D SCM2_MACMU
5CM2_M C07370
DT 01-NOV
DT 01-NOV
DT 02-FEB
DE Growth
DE HOTOMON
GN GH2.
OS MARMAN
OC BUKATY
OC CETCOP
OX NCBL_T
RN [1]
RR [1]
RR GOLOS
RA GOLOS
RA GOLOS
RA GOLOS
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RA GOLOS
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                              Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Cloting of four growth hormone/Chorionic somatomammotropin-related complementary decyptibonucleus acids differentially expressed during pregnancy in the rates monkey placenta.";
Endominology 133:1744-1752(1993).
-! FDWCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and chor tissues to secrete IGF1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 FPIIPLSWLFNTAVFRAHHLHKIAFDTYPKLEBAYLPKECKYSFLKNPQTSLCFSESIPT
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01-APR-1988 (Rel. 07, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lactogen precursor (Choriomammotropin) (Chorionic somatomammotropin),
CSH1 AND CSH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Sukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selby M.J., Barta A., Baxter J.D., Bell G.I., Eberhardt N.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed in the placenta.
-!- SIMILARITY: BELONGS TO THE SONATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 396; DB 1; Length 21/
Pred. No. 3 9e-34;
"---rohes 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 200 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 | 201 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PSNREETQQKSNLFLLRTSLLLLQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2:7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS: PRO0836; SOMATOTROPIN.
PROSITE; PSO0266; SOMATOTROPIN.1: PROSITE; PSO0338; SOMATOTROPIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (GENE CSH1).
MEDLINE=85030426; Pubmed=6208192;
MEDIINE-94008724; PubMed-8404617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U02293; AAA03391.1; -. EMBL; L16555; AAA20180.1; -.
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84.6%;
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es 77, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; 167411; 167411
HSSP; P01241; 1HGU.
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X Strusberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,

A Strusberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,

A Rausher R.D., Collins F.S., Warner C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Scharter C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Nabin G.M., Engy L.,

B Diatchenko L., Marusina K., Farmer A.A., Man J., Scherro T.E.,

A Stapleton M., Soarcs M.B., Bonaldo M.F., Casavant T.L., Scherro T.E.,

B Stapleton M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.T.,

B Bosak S.A., McEwan P.J., McKernan K.J., Mark J.A., Gunarathe P.E.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.K.,

A Nilaton D.K., Muzny D.M., Sodergron E.J., Liu X., Glibbs R.A.,

Fahey J., Helton E., Kettenan M., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterflield Y.S.N., Kroywinski M.L., Salakka C., Smarius D.E.,

Robersation and initial analysis of more than No. 101-1011
"Analysis of a major haman chorionic somatomanmentopin gene. Evidence
                                                                                                                                                                                                                                                                                          Chen E.Y., Lizo Y.C., Smith D.H., Barrera-Saldana B.A., Gelinas R.E.
Seeburg P.E.;
                                                                                                                                                                                                                                                                                                                          "The human growth hormone locus: nucleotide sequence, biology, and evolution.";
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-83160916: PubMed-6306056:
Harrera-Sadduna H.A., Seebarg P.H., Saunders G.F.;
Fro structurally different genes produce the same secretes human placental lactores formone.";
J. Biol. chem. 256:3787-3733(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                       The human growth hormone gene family: nucleotide segmences snow recent divergence and predict a new polypeptide hormone. ",
                                                     SECUENCE FROM N.A. (GENE CSE2).
MEDLINE-87161235: PubMed-3030680.
Hirt H., Kimelman J., Birnbaum M.J., Chen B.Y., Soeburg P.B.,
Eberhardt N.E., Barta A.;
"The human growth formone gene locus: structure, evolution, and
allelic variations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li C.H., Dixon J.S., Chung D., *Amino acid sequence of human chorienic sematemannetropin.", Arch. Biochem. Riophys. 155:95-113(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. 6.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (GENES ISH) AND CSHI).
MEDLINE-89307277; PUDMed-2744769;
              for two functional promoter elements.";
J. Biol. Chem. 259:13131-13138(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-73261971; PubMed-4712450;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83182010; PubMed-7169009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=72016313; PubMed-5286363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-78071761; PubMed-593368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 50-217 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 270:494-499(1977).
                                                                                                                                                                                                                                                                                                                                                     Genomics 4:479-497(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:239-243(1982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 27-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           somatomammotropin.
                                                                                                                                          DNA 6:59-70(1987)
                                                                                                                                                                                                                                                                                                                                                                                                              Seeburg F.H.;
                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
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                                                                                                                                                                           INTERCHAIN (WITH C-215 IN A DIMER).
INTERCHAIN (WITH C-208 IN A DIMEK).
P -> A (IN CSH2).
/FIId-VAR_007155.
                                                                                                                                                                                                                                                                                                                      MISCHILANECUS: THE SEQUENCE OF CSHI IS SHOWN. SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.1%; Score 381; DB 1; Length 217; 62.0%; Pred. No. 1.4e-32;
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Storwood L.M., Handwerger S., McLaurin W.D., Lanner M.; "Amino-acid sequence of human placental lactogen."; Nature New Biol. 233:59-61(1971).
                                                                                                   Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M., Nature New Biol. 235:64-64(1972).
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235B0DC7A713F431 CRC64;
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/FIG-VAR_007167.
I -> T (IN REF. 9).
MISSING (IN REF. 9).
MISSING (IN REF. 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Formone, Placents, Multigene family, Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 NREETQOKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LACTOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pram; Proutos; normone; 1,
PROSITE; PS00266; SOMATOTROPIN_1; 1,
PROSITE; PS00338; SOMATOTROPIN_2; 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM: 150200; -. GO: 0007555; F:pregnamcy; TAS. InterPro; IPR061400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: V00573; CAA23836.1; -
EMBL: J00289; AAA98747.1; -
EMBL: M02401; AAA52115.1; -
EMBL: M1584; AAA52116.1; -
EMBL: J03071; AAA5255.1; -
EMBL: J00118; AAA98621.1; -
EMBL: BC005921; AA42717.1; -
EMBL: BC005921; AA420756.1; -
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                                                                                                                                                             INTERCHAIN DISULFIDE BONDS
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25920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; #GNC:2440; CSH1.
Genew; #GNC:2441; CSH2.
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95
116
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215
208
215
3
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PIR; C32435; LCHUC.
HSSP; P01241; 1A22.
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95
116
134
217 AA;
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Matches 73: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
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DISULFID
DISULFID
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                ERRATUM.
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FPAMPLSSLEANAVIRAGEBHELAADTYKEFERAYIPFGORV-FLONAOSIGGESEVIPT 59
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"Structural studies of tryptic peptides from large cyanogen bromide fragments of sei whall opticate borearis) somatotropin.";
iragments of sei whall proper a borearis) somatotropin.";
Bioorg. Khim. 4:1589-1599(1978).
-:- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPTIPLSRLFDNAMLRAHRIJIQLAFDTYQEFEEAYIPKEÇKYSFLQNPQTSLSFSRSIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linzer D.1.H., Talamantes F.; "Nucleotide sequence of mouse prolactin and growth hormone mRNAs and expression of these mRNAs during pregnancy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae; Mus.
                                                                                                           Balaenophera borealis (Sei whale).
Bukaryota, Metazoa, Chordata, Craniata: Vertebrata, Euteleostomi.
Mammalia: Butheria: Cetartiodactyla, Cetacea, Mysticeti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1. SUBCELLULAR LOCATION: Secreted.
-1. SIMILARITY: BELCINGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
PIR; PN0140; PN0140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
09FBFF60B14A75D6 CRC64;
                                                                                                                                                                                                                                                    MEDLINE=83000569; PubMed=7115813;
Yudaev N.A., Parkov Y.A., Bulatov A.A., Osipova T.A.;
"Amino acid sequence of solwhale somatotropin.";
Amino acid 47:1059-1069(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.4%; Score 367.5; DB 1;
67.0%; Pred, NO. 5.2e-25;
live 14; Mismatches 15;
ClearI-1993 (Rel. 27, Created)
61-667-1993 (Rel. 27, Last sequence update)
68-1657-1993 (Rel. 41, Last annotation update)
SomatoLropin (Growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 06, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (2 PSNREETQOKSNUELLRISHLINGSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somatetropin precursor (Growth hormene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMIT PF01103; hormone: 1. FROSITE: PS00256; SCMATCHROPIN_1; 1. PRCSITE: PS00338; SCMATCHROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; 1PR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85261358; PubMed-2991252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                        Balwenopterídae, Balwenoptera.
NCBI_TaxlD=9768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 188 E
190 AA; 21835 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rukaryota: Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rest Local Similarity 67.09
Matches 61, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSILE; rocci
Hormone: Pituitary.
52 :63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01241: 1AXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01 JAN-1988
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOMA_MOUSE
P06880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GH1 OR GH
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                                                                                                                                                                                                                                         SECUENCE
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SOMA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PPT 1PLSRLFDNAMLKAHRLHGLAFOTYGEFEEAY;FKKOKYSFLONFGTSLSFSESIFT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 FPAMPLSSLFANAVLKACHLHQLAADTYKEFERAYTPEGGRYS-1QNAQTAFCFSETIFA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endocrinology 129:2965-2971(1991).

-i- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete (GF-I). It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and proliferation synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scien
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92063850; PubMed-1954881;
Southard J.N., Sanchez-Jimenez F., Campboil G.T., Talamantes F.;
"Sequence and expression of hamster prolactin and growth hormone
messenger RNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATCHROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is: Indels
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BY SIMILARITY.
3869GE32AB6F1166 CRUSGA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.18; Score 310.5; DR D
67.08; Pred. No. 3e-25;
                                                                                                                                                                     01-0CT-1954 (Rel. 30, Greated)
01-0CT-1994 (Rel. 30, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILL FILLS THE FILL GAME FOR THE FILL OF SWINGPVO 116
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                      89 NMEETOOKSNIELSEISHIJJESWLEPVR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
                                                                                                                                                                                                                                         Somatotropin precursor (Grewth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE DESTRUCTOR
                                                                                                                                                                                                                                                                               Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS00266, SCMATOTRCPIN_I, 1. PROSITE, PS00338, SCMATCTRCPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946; IBST.
IPROC1400; Somutetropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S66299; AAB20368.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hormone, Pithitary, Signal.
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                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216
189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPROC1400; Soi
Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, B49159, B49159.
HSSP, P01246, IBST.
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216 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCB1_TaxID-10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissmes.
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P33092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61:
                                                                                                                             SOMA_MESAU
P37886;
                                                                                                                                                                                                                                                           GH1 OR GH
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STATE THE STATE OF ST

SPOUENCE

Matches Best

g ò RESULT 1: SOMA_BALBO

SIGNAL

CHAIN

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1; Gaps

Indels

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DISULFID
                                                                                                                                                                                                                                                                                            hormone."
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                                                                                                                                                                                                               hormone.
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   9
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration decreen the SWISS institute of Michidormatics and the FWAN citation. the European Richformatics Institute. There are no restrictions on its use, by non-prefit isaliations as long as its content is in no way.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FPTIPLSRLFDNAMLRAJRLHQLAFOTYQEFEBAYIPKRQKYSFLQNPQTSLSFSESIFT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to scretch 109-1. It stimulates both the differentiation and politeration of myobiasts, it also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l, Gaps
                                        MEDLINE-56194803; PubMed-8347448;
Das P., Meyer L., Seyfert 4.-M., Brockmann G., Schwerin M.:
"Structure of the growth bormone-encoding gene and its promoter in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eguus caballus (Borse).
Eukaryota, Metazoa, Chordata, Craniata, Vertchrata, Euleleostom,
Mammalia, Eutoria, Perissodactyla, Equidae, Equis.
                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOIROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.8%; Score 364.5; DB 1; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                98666A3AE25D65FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.2e-24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JJL 1986 (Rel. Cl. Created)
01-NOV-1995 (Rel. 32, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pituitary;
MEDLINE-94266171; PubMed-8206392;
Ascacio-Martinez J.A., Barrera-Saldana H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                SCMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     PY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00103: hormone, i.
PROSITE: PS00266; SOMAIOTROPIN_:: 1.
PROSITE: PS00338; SOMAIOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT
Biol. Chem. 260:9574-9579(1985)
                                                                                                                                                                                                                                                                                                           PTR, B23911, STMS.
HSSP, P01246, 1337.
MGD, MGI:95707, Gh.
InterPro, IPR001400; Somarotropii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                216 AA; 24716 MW;
                                                                                                                                                                                                                                                                                      EMBL: X02891; CAA26650.1; -:
EMBL: 246563; CAA86653.1; -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.88;
                                STRAIN FZIDO: TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                           Hormone: Pituitary: Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 64.8
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                      Gene 169:209-213(1996).
                                                                                                                                                                                                                                                                                                                                                                                                              216
189
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                       SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOMA_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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SOMA_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nother, 7. 199:19-24(1968).

Brother 1. 199:19-24(1968).

Finction: Plays an important role in growth control. Its major rele in stimulating body growth is to stimulate the liver and ciber lissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in mescle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zakin M.M., Poskus E., Dellacha J.M., Paladini A.C., Samtome J.A.; "Amino acid sequences around the cystine residues in equine growth
                                                                                                                                                                                                                                                                                                                                                                                                     Santome J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cliver L., Hartree A.S.:
'Amino acid sequences around the cystine residues in horse growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                          Zakin M.M., Poskus E., Langton A.A., Ferrara P., Santome J.A., Dellacha J.M., Paladini A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SURCELLUIAR LOCATION: Secreted.
-1- SIMILARITY: BELON'S TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                            PRELIMINARY SEQUENCE OF 27-216.
MEDIINE-74020362: Pubbed=4447849;
Zakin M.M., Poskus E., Dellacha J.M., Paladini A.C.,
"The amino acid sequence of equine growth hormone.";
"Sequence of a cDNA encoding horse growth hormone.";
Gene 143:299-300(1994).
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                                                                                                                                                                                                                               "Primary structure of equine growth hormone."; Int. J. Popt. Protein Res. 8:435-444(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCMATOTROPIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-68368390; PubMed-4876100;
                                                                                                                               MEDLINE-77005410: PubMed-965151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 68-95 AND 183-216.
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HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 34:353-355(1973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FESS Lett. 25:77-82(1972).
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189
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nes 59; Conserv
                                                                                                SEQUENCE OF
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Conservative
                                                                                                                                                                                                                                                                                                                                                                 Nature 270:485-494(1977).
      norvegious (Rat)
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169
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78 1
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216 AA;
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HSSP; P01246; IBST.
InterPro; IPR001400
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Matches 59; Conserv
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                                         Nammalla; Euthern
NCB1_TaxID=10116;
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      between the Swiss Institute of Bioinformatics and the EMEL cutstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
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-!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STAX.N-New Zealand white;
MEDLINE=9601643; PubMed=7590276;
Mallis O.C., Wallis M.;
"Cloning and characterisation of the rabbit growth hormone-encoding
                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertobrana, Euteleostoc.,
Mammalia, Eutherla, Lagomorpha, Leporidae, oryminiagus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLUIAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS IO THE SOMATOTROPIN/PROLACITIN PAMILY.
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SCHATGTRCPIN.
BY SIMILARITY.
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6EC19748199F9375 CRC54.
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21-JUL-1986 (Rel. 01, Last. Sequence update)
28-FEB-2003 (Rel. 41, Last innotation update)
Somarctropin precursor (Growth hormone).
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  216 AA
                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annetation update
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                                                                                                 Somatotropin precursor (Growth hormone)
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InterPro, IPR01400; Somatotropin, Pf30103; hormcoe, 1.
PR017S; PR0086; SCMATOTROPIN, PROSITE; P300256; SCMATOTROPIN_1: 1.
PROSITE; F300338; SCMATOTROPIN_2: 1.
                                                                                                                                         Oryctolagus coniculos (Rabbit).
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mes 59; Conservative
  STANDARD;
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216 AA:
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P01244;
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Detween the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its make by non-profit institutions as long as its content is in no way additionables statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seeburg P.H., Shine J., Martial J.A., Baxtor J.D., Goodman H.M.;
*Nucleotide sequence and amplification in bacteria of structural gene
for rat growth cormone.";
                                                                                                                                       SEQUENCE FECM N.A.
MEDIINE-82059526: PubMed-6272224;
Page G.S., Smith S., Goodman H.M.;
PubM sequence of the rat growth hormone gene: location of the 5'
"UNA sequence of the growth hormone mRNA and identification of an internal gransposon-like element.";
Enkaryota; Metazoa: Chordata; Craniata: Vertobrata; Buteleostomi;
Mammalla; Butheria: Rodentia; Scinrognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
MEDLINE=82060155; PubMed=6946433;
Barta A., Richards R.I., Baxter J.D., Shine J.;
Parta A., Etchards R.I., Baxter J.D., Shine J.;
Primary Structure and evolution of rat growth hormone gene.";
Proc. Natl. Acad. Sci. U.S.A. 78:4867-4871(1981).
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BY SIMILARITY.
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F -> L (IN REF. 2 AND 4).
W; CABF49DC0B2A226C CRC54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuroimmunomodulation 2:108-114(1995).
                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 9:2087-2164(1981).
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Pfam: PF00103; hormone; 1.
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MEDLINE-96056604; PubMed-8521139;
Rohn W.M., Weigent D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=78071760; PubMed-339105;
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September 15, 2003, 11:54:30 ; Search time 35:5427 Seconds (without alignments) 660.520 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c: 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp.bacteria.*
sp.tungi.*
sp.tungi.*
sp.human.*
sp.invertebra.e.*
sp.mammal.*
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		Ouery Match Length DB		217	245	217	212	217	217	217	202	217	216	216	216	2:6	204	216	217
•	*	Cuery		92.8	8.68	84.5	84.3	84.3	81.1	74.0	71.6	67.7	65.2	T 53	64.1	63.5	63.3	63.3	63.2
		Score) !	435	422	397	396	396	381	348	336.5	318	306.5	301.5	301.5	298.5	297.5	297.5	297
		Result No.		П	7	3	₹	S	9	7	æ	6	10	11	12	13	14	15	16

C9tu21 capra hircu O9tqw9 bos indicus O95hqw9 cavia porce O95hq9 cavia porce O95hq9 traqulus ja O9bec0 traqulus ja P24451 homo sapien O95hq9 rus scrofa Q28677 sus scrofa Q9540 canis famil O9pu72 cynops pyrr O9bu72 cynops pyrr O9bu74 qalaqo cras Q1386 amia calva Q8axx anquilla an Q8axx anquilla an Q8qfm8 clarias bat Q90x81 carassius a Q98rt megalobrama C8qqi heteropneus O90x01 mylopharama Q8uv62 siturus asconeus and mylopharama Q8uv62 siturus asconeus opense mylopharama Q8uv62 siturus asconeus opense mylopharama O8uv62 siturus asconeus opense ope	090w26 carassius a 08ax85 carassius a 098sr7 cyprinus ca) Euteleos.comi; Atclinac; Ateles.	ana B.; ene in three tabascs. CRC64;	imilarity 92.6%; Score 435; DB 6; Length 217; Conservative 4; Mismatches 3; Indels 0; Gaps 0; FPTIPLSELEDMAMLEAHRLHQLAPDTYOEPERAVIPKEOXYSFLONPOTSLSFSESIPT 61
	S INHENDS	PRI; 217 AA. Created) Last sequence undate) Last annotation update) ded spider monkey). a; Craniata; Vertebrata; s; Platyrrhini; Cebidae;	NCSIGALLOSCO.; NCSIGALLOSCO.; SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE ERGALVELD., Santiago D., Barrera-Saldana Trdepocident dipplication of the growth hormone gene Anthropoidean lineages."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databa EMBL, NCS 1786.1; - LARDL. ANALY2286.1; - LARDL. PROOLIGS. HORMONE; L. Fram: PROOLIGS. HORMONE; L. PROSITE: PSCOUSE6; SOMATOTROPIN.]; 1. PROSITE: PSCOUSE6; SOMATOTROPIN.]; 1. SEQUENCE 217 AA; 24894 MW; 425829FF41EEAAE6 CRC6	Score 435; DB 6; Le Pred. No. 3.5e-41; 4; Mismatches 3; LHQLAFDTYQEFEBAYIPKEQK HILLHIHHHHHHHH LHQLAFDTYQEFEBAYIPKEQK CLLIQSWLEPVQ 92 HHHHHHHH LHHHHHHHHHHHHHHHHHHHHHHHHHHH
0997U21 0997U8D 0997UGD 0997UGD 0998B9 098B9 098B9 099702 099702 099702 099703 090703 090703 090703 090703 090703 090703	090W2 088XS 0988R 0988R	PRT; reate ast s ast a d spi cran	iago D., the grr EMBL/Ge rropin. tropin. PPIN_1; PPIN_2;	imilarity 92.6%; Score 435; Conservative 4; Mismatch 4; Mismatch 111111111111111111111111111111111111
		20, 20, 23, 23, han	Sant 1 of the the 5.1; 5.1; 7.1 OTRC	6%; 3%;
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MEDLINE-94008724; PubMed-8404617;
Golos T.G., Durching M., Fisher J.M., Fowler P.D.,
Cloping of four growth hormone/chorienic sematurammotropin-relitation
complementary decayribonaciera acids differentially expressed differential pregnancy in the rhesus monkey placental;
pregnancy in the rhesus monkey placental;
Endocrinology 13:1744-1752(1993).
EMBL: L16554: AAA1841.1: ...
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Carlsson L.M.S., Carlsson 3.,
"Cioning of two movel growth hormone transcripts expressed in luman
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Buraryola Motacca, Chordala: Cianíata, Vertebrala: Enteleostomo:
Mammalia: Eutheria: Primatos: Catarrilni: Gencopithonidae:
Cercopitheringo: Macaca.
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Mammalia: Eutheria: Primatos: Catarrhini; Hominidae: Homo:
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Local Similarity 92.3% Pred. No. 1.2e-39;
nes 84; Conservative 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27101 MW; 14CC7F8CD75D9108 CRC64;
                                                                                                         01-JAN-1998 (TrEMBLrel. 65, Created)
01-JAN-1999 (TrEMBLrel. 65, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HOB-COLLAR GRAND PROGRESSION PROCESSION HOB-V.
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Last annotation update;
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J. Clin. Endocrinol. Metab. 83:2678-2865(1998).
EMBL; AF006061; AAB71829.1: -.
HSSP; P01241: 1A22.
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Pfam: PF00103; hormone: 1.
PROSITE: PS00266; SOMATOTROPIN_1: 1.
                                                          PRT.
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MEDLINE-98373737; PubMed-9709963;
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61-NOV-1996 (TYEMBLYEL) CL
01-MAR-2003 (TYEMBLYEL) 23
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                                                               PRELIMINARY:
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                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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RESULT 3
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                                                                                                                                               28 PSVPLSRLFDNIRMQARREHQLAFDTYQEFEKTYIPKEKKHSLMGNPQASFCFSESIPIP 87
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"Cloning of four growth hormone/chorionic somatomamotropin-related
complementary deoxyribonucleic acids differentially expressed during
pregnancy in the rheeus monkey placenta.";
Endocrinology 133:1744-152(1993).
EMBL. 116583, AAA18440.1;
InterPro: IPR001400: Somatotropin.
                                                              Gaps
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Mammalia; Euthoria; Primates; Catarrhini; Cercopithecidae;
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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  Length 217;
  Score 397: DB 6: Length 21
Pred. No. 6.90-37;
8: Mismatches 7: Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAV-2003 (TrEMBLrel. 23, Last annotation update)
Somacctropin 2 precursor (Growth hormone 2) (Fragment).
Macaca mulatta (Khesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 AA; 24525 MW; 27BC91106256E6F5 CRC64;
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23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                      212 AA
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01-NOV-1996 (TrEMBLRel. 01, Last seq
01-MAR-2603 (TrEMBLRel. 23, Last anno
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PRCSITE; PS06338; SCMATOTROPIN_2; 1.
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MEDILINE-94008724; Pubmed-8404617;
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TISSUE=Midpregnancy placenta;
     84.5%;
0uery Match
Best Local Similarity 83.39
Matches 75, Conservative
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NCBI_TaxID-9544;
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SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth hormone.
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COMNIDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PTIPLSRLFDNAMLRABRAHOLAFDTYOBRBBAYIPKEQKYSFLAMFOISLSFSSKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel, Cl, Created)
01-NOV-1996 (TrEMBLrel, Cl, Last Sequence applate)
01-NAR-2003 (TrEMBLrel, 21, Last annotation applate)
Chorlonic somatomanmetropin CS-2 (Chorlonic sematonammetropin hurmenn
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                 Golos T.G., Durning M., Fisher J., Towler P.D.; "Cloning of four growth hormone-Cohorine somatomammotropin-related complementary deoxyribonacleic acids differentially expressed during preparancy in the rhesus monkey placenta."; Endocrinology 133:1744-1752(1993).

EMBL: L16552: AAA18839-1; -...HSSP; P01241: 1AXI.
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MEDIAHE-89307277; PubMed-1744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Selicas R.E.
Seeburg P.H.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The human growth hormone locus: nucleoride sequence, blolony, and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDEINE 91102558: PubMed*1980158:
Nencak-Jones C.L., Phillips J.A. 111.:
"Bot spots for growth hormone gene deletions in homologous regions
outside of Alu repeate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazon, Chordata, Craniata, Vertebrata, Entelecstori:
Mammalia, Eutheria, Primutes, Catarrhini, Rominidae, Bomo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.3%; Score 955; DB 6; Length 217; 52.2%; Prod. No. 8.96-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.:
Strausberg R.:
Submitted (JUL-2002) to the EMBL/GenBank/DVBL databases.
EMBL; 503071: AAA52553.1;
EMBL; BC022044: AAH32044...
EMBL; BC035965: AAH35965.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  InterPro; IPR001430; Somatotropin.
Pfam: PF0013; Normoue: 1.
PRINTS; PR00834: SOMATOTROPIN.
SP005TE; PS00338; SOMATOTROPIN. 2: 1.
SF0UENCE 217 Aa: 24942 MW; FF5AAB6915131F2BG CR054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.3%; score 55.5.
Best Local Similarity 82.2%; Pred. No. 8.96*
Matches 74; Conservative II: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNIEETQQKSNIELLRISELLIQSWEEVQ ::?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 SNREETQQKSNLELLRISTLLIQSWDEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001400: Somatotropin, Pfan, PF00103: Normance: 1. PRINTS: PR00836; SOMATOTROPIN, PROSITE; PS00266; SOMATOTROPIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
MEDLINE-94008724; PubMed-6404617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 250:1745-1748(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 4:479-497(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Placenta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCB1_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              014407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                            29 TVPLSRLEDHAMLQAHRAHQLAIDTYQEFEETYIPKDQKYSFLHDSQISFCESDSIPTPS 88
                                                                                                                                                                                                             4 TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ateles geoffroyi (Plack handed spider monkey).
Enkaryota, Metazoa: Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini: Cebidae; Atelinae; Ateles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutcleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROVINCE FROM N.A.

Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;

Rocolent diplication of the growth hormone gene in three Antiropoidean lineages.";

EMBL, AF374235: AAL72287.1;

EMBL, AF374235: AAL72287.1;

THEPPON IPPONION: Somatorropin.

Pran; PF00103: Jornane: L.

FRINTS: PROUGE: SUMATOTROPIN.

PROSITE: PS00266: SUMATOTROPIN.];

PROSITE: PS00266: SUMATOTROPIN.];

PROSITE: PS00266: SUMATOTROPIN.];

PROSITE: PS00266: SUMATOTROPIN.];
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%; score 348; DB b; Length 217; 75.8%; Pred. No. 2.4e-31; Live 8; Mismatches 14; Indels
                                                                                     Length 217;
PRCSITE; PS00338; SCMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24994 MW; 39FAACDDB6B2E951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25293 MW; 741745A1B75C653E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0:-MAR-2002 (TremBirel, 20, Created)
0:-MAR-2002 (TremBirel, 20, Last sequence update)
0:-OCT-2002 (TremBirel, 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1996 (TrEMBLrei. 05, Created)
1-JAN-1998 (TrEMBLrei. 05, Last sequence update)
01-07N-2002 (TrEMBLrei. 21, Last annotation update)
Placental growth hormone 20kDa isoform precursor.
                                                                                     81.1%; Score 381; DB 4; 182.0%; Pred. No. 4.4e-35; iive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PENKEEVUAKSSLEILHISILITQSWLEPVQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PSNRBETQQKSNLELLRISILLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AA
                                                                                                                                                                                                                                                                                                                                                             64 NREETQQKSNLELLRISLLLIGSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Term placenta;
MEDLINE-98373737; PubMed-9709963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata,
Mammaila, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bost Local Similarity 75.8 Matches 69, Conservative
                                                                                                                    Best Local Similarity 82.0
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Delphinus delphis (Saddleback dolphin) (Black soa dolphin).
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Cetarticdactyla: Cetacea: Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PPTIPLSRLFUNAMERAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONPQ1SLSFSSSIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Manion 2., Wallis C.C., Wallis M.; "Clouing and characterisation of the GH gene from the common dolphin
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDINED-1924177; MEDINE-992466 A., NewO. E., Wallis M.; "Cloning and characterisation of the gene encoding mole rat (Spalax "Cloning and characterisation of the gene encoding mole rat
                                                          01-A3G-1998 (TrEMBLrei, 07, Created)
01-A3G-1998 (TrEMBLrei, 07, Last sequence update)
01-AMR-29G3 (TrEMBLrei, 03, Last annotation update)
scowt: hormone precursor.
Stowt: hormone precursor.
Stylank leucodon ehrenbergi (Ehrenberg's mole rat).
Stylank leucodon ehrenbergi (Ehrenberg's mole rat).
Wakaryota, Metazob: Chordata: Craniata, Vertebrata; Futeleostomi:
Mammalia; Futheria: Rodentia; Sciurognathi: Muridae; Spalacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oucry Match
Best Local Similarity 65.9%; Pred. No. 1.2e-26;
Matches 60; Conservative 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (De)phinus delphis).":
Submitted (JUN-2002) to the EMBL/GenBank/DDRJ databases.
EMBL; AJ492191; CAD37292.:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 POTENTIAL.
216 GROWTH HORMONE.
24627 MW: EEABBAS23BAOADFE CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-00T-2002 (TrEMBLrel, 22, Created)
01-00T-2002 (TrEMBLrel, 22, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
GROWTH HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 216 AA
           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ditactory IPR001400; Somatotropin.
Pfam. PF00103; hormone: 1
PR0118; PR00636; SomaToTROPIN.
PROSITE: PS00266: SOMATOTROPIN. 1;
PROSITE: P506338; SOMATOTROPIN_2: 1.
     PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
           PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
216
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                                                                                                                                                                                                                                                                                    NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID+9728:
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                                                                                                                                                                                                                                                                   Nathospalax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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           qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PTIPLSRLEDNAMLRAGBELHQIAFDTYOBFSEANIPKEGKYSFLQNPQISLSFSFSIFFF + 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FPTTPLSRLFUNAMIRAJRLHQLAFDTYQEFEEAYIPKFOKYSFLONPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHLP6.
Callithrix jacchus (Common marmosel).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Esteleostomi:
Mammalia: Eutheria: Primates: Platyrrhini: Callitrichidae: Callithrix.
NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mallis O.C., Wallis M.;

Mallis O.C., Wallis M.;

Characterisation of the GH gene cluster in a new world medkey. the GH farmoset (Callithrix jacchus).";

J. Mol. Endocrinol. 0:00(202).

EMBL; A1489811; CAN34012.1;

InterPro: IPR001400: Somatotropin.

Pran: PR001401; hormone. 1

PRINTS; PR00386; SOMATOTROPIN.

PROSTE: PSC0338: SOMATOTROPIN.
                                Carlsson L.M.S., Carlsson B.; "Cioning of two newel around transcripts expressed in homen
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.5%; Score 336.5; DH 4; Length 202; Best Local Similarity 76.9%; Pred. No. 4.46-50; Matches 70; Conservative 3; Mismatches 3; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROWTH HORMONE-LIKE PROTEIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.7%; Score 318; DP h; Length 217;
68.9%; Pred. No. 5.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5ECF148798278F1A CBC64;
                                                                                                                                                                                                                                                                                                                                                                       SIĞNAL 1 26 POTENTIAL.
SEQUENCE 202 AA; 23128 MW; 36B64D011A919706 CRC64;
     Svenssor P.A., Jansson J., Thik R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                     placenta.;
J. Clis. Endocrinol. Metab. 83:2878-22885(1958).
EMBL. APCOGODO, AAR71828.1;
InterProj. 1PR01403. Somatoiropin.
Pfam: PP00123. hormone; 1.
PR01Es. PR00836; SOMATOTROPIN.
PROSITE: PS00266; SOMATOTROPIN.
PROSITE: PS00386; SOMATOTROPIN.
PROSITE: PS00388; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mistatores
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217 GR
7 25177 PW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.99
Les 62, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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27
217 AA;
Boguszewski C.L.,
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Q8MI74;

08MI74

RESULT 9 08M17

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SOUR SET THE SOUR SOUR SET THE SOUR SOUR SET THE SOUR SET

Best Loc Matches

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61

1; Gaps

us-09-423-100-2.rspt

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PRINTS; PRO0836; SOMAICTROPIN.
PROSITE; PS00266; SOMAICTROPIN.1; 1.
PROSITE; PS00338; SOMAICTROPIN.2; 1.
SEQUENCE 216 AA; 24682 MW; FC2A06DA02536B18 CRC64;
 Pfam: PF00103; hormone: 1.
                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                       095205
095205;
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195205
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                                                                             2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFERAYIPKEQKYSFLQNP075LSFSES1PT 6.
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27 FPAMPLSSLFANAVIRAGHAQLAADTYXBFERAYIPSGGRYS-TGNTGAAFGPSETTPA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFHHAYIPKEQKYSFLQNPQTSLSFSESIFT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                          Aliuropoda melanoleuca (Giant panda).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Esteleostomi:
Mammalia: Buthoria, Carnivora, Pissipedia: Grsidae, Alluropoda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Entelcostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEGUENCE FROM N.A. Number S.A.; Nguyen T.N.K., Liebhaber S.A.; "Mouyen T.N.K., Liebhaber S.A.; "Mouse Growth Hormone Locus: Nucleofide Sequence and Phylomenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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Best Local Similarity 64.8%; Pred. No. 4.3e-26;
                         64.18; Score 301.5; DB 6; Longth 216; 64.88; Pred. No. 4.36-26; Live 14; Mismatches 17; Indels 1
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Pituitary;
Liao M., Zhu M., Zhang A.;
Clonching and expression of GDMA encoding arouth hormone from
Alluropoda metapholouca.";
Submitted (AUG-2002) to the EMBL/SenBank/NOSH Jatabases.
EMBL: AF540336: AAN77228.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analyses.";
Submitted (AUG-1995) to the EMBL/GenHark/PGBJ calabases
EMBL: 04362: AAC99968.1; -
HSSP: P01241: 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 26 POTENTIAL.
216 AA: 24383 MM: 44EC17E04450B056 CRC64;
 IEC467A84CCFEB02 CRC64;
                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TREMBLrel. 23, Last annotation update)
Growth hormone predureor.
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23, Last annotation update)
                                                                                                                                             62 PSNREETOOKSNLELLRISLLLIQSWLEPVO 92
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  24509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Conservative
                                                   59; Conservative
                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
  216 AA;
                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth hormome.
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SEQUENCE
                          Query Match
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Q9R2C3:
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QBHYE5
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                                                   Matches
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                                                                    Gaps
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Lacriax M.C., Devinoy B., Servely J.L., Puissant C., Kann G.;
Lacriax M.C., Devinoy B., Servely J.L., Puissant C., Kann G.;
Lacriax M.C., Devinoy B., Servely J.L., Puissant C., Kann G.;
and cellular localization of the protein.";
Endocarinology 137:4886-4892(1996).
EMBL: U49663; AAC46679.1;
HSSP: P01241; 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazóa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidoa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TEMBLIEL 15, Created)
01-0CT-2000 (TEMBLIEL 15, Last sequence update)
01-MAR-2003 (TEMBLIEL 23, Last annotation update)
Growth hormone precursor.
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
                                                                ;
Query Match 63.5%; Score 298.5; DB 11; Length 216; Pest Local Similarity 63.7%; Pred. No. 9.4e-26; Matches 58; Conservative 14; Mismatches 18; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61-F28-1997 (TrFMBLrel. 02, Created)
61-F28-1997 (TrFMBLrel. 02, Last sequence update)
61-F28-1997 (TrFMBLrel. 23, Last annotation update)
placenclal growth formone (Fragment).
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                                                                                                                                                                                                                                                                             74 PTSKNEAQQKSDLELLRISHLIQSWLGPLQ 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001400; Somatotropin.
Pfam: PF00103; bormone: 1.
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Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRFLIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae: Caprinae; Ovis
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Mammalla, Butheria, Rodontia, Hystricograthi, Cavildae, Cavia.

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2 FPT (PLSRLF) DNAME, RAERLHQLAFDTY QEFERAY TERROKYSFLON PQTSLSFSES [FT 4]
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Best Local Similarity 63.7%, Pred. No. 1.26-25;
Matches 58; Conservative 14; Mismatches 18; Indels 1; Gaps
                                                                                                                                                           SEQUENCE FROM N.A.

Odorico D.M., Fuller E.J., Herinaton A.C.;
Cloning and sequence of quincy pig growth homome (88).";
Submitted (FBS-2006) to the BMFL/Genback/Orded dathases.
BMBL: AF233853: AAF36409.1;
BMBL: AF233853: AAF36409.1;
InterPro; IPRGO1409; Somatciropin.
Prints: PRO0836; SOMATCHKPIN.];
PROSITE: PSO0836; SOMATCHKPIN.];
PROSITE: PSO0836; SOMATCHKPIN.];
PROSITE: PSO0838; SOMATCHKPIN.];

        SIĞNAL
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        26
        POTENTIAL.

        CHAIN
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        SRCWTH HORMONE.

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        AA; 24822 PW; 45596BEL19B0BOD3 CROS4;

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225.942 Million cell updates/sec
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/SIDSI/gcgdata/geneseqy-cch:/AA1965.DAT:-
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| S1DSI/gcgdala/qeneseg/genesegp.emb./AA1996.DAI:
| S1DSI/gcgdala/geneseg/genesegp.emb./AA1996.DAI:
| S1DSI/gcgdala/geneseg/genesegp.emb./AA1999.DAI:
| S1DSI/gcgdala/geneseg/genesegp.emb./AA1001.DAI:
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Gercore version 5.1.6 copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 150%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Sequence encoded b Proinsulin protein Modified human ins hpl. Homo sapiens Yeast alpha-factor Synthetic proinsul Human proinsulin p Human proinsulin p Human proinsulin p Sequence encoded b Sequence of preprosecuence of preprosec	Human preproinsull Human preproinsull Human insulin. Ho Human insulin. Ho Human proinsulin. Ho Human proinsulin preproinsulin Human preproinsulin Human preproinsulin Human preproinsulin Human proinsulin Human proinsulin Human met. Arg proi Human met. Arg proi Human met. Tyr proi Human proinsulin Human preproinsulin	Signeties; hormone.	de y or enzymatically peptide residue"
AAP6109 14 AAR323 11 AAR336 14 AAR336 14 AAR336 10 AAR306 20 AAV080 15 AAR688 21 AAB1305 2 AAP1005 2 AAP1005 3 AAP1005 5 AAP1005	20 AAY66608 21 AAB26765 22 AAB26765 22 AAY44367 22 AAA74367 0 22 AAC56777 0 22 AAC56034 0 23 AAG56034 7 21 AAY65788 1 20 AAW81856 1 20 AAW81856 1 20 AAW81856 1 14 AAR3575 8 14 AAR3575 8 14 AAR3575 6 20 AAV18605 6 20 AAY18605 6 20 AAY18605 6 21 AAY1861 8 14 AAR3676 8 14 AAR3676 8 21 AAY1861 9 21 AAY1861 9 21 AAY1861	ALIGNMENT Lin: 65 AA. ry) in precursor.	on/Qualifiers crain B connecting peptide chain A F-NH2-R H or a chemically ble AA residue or pe
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1 FVNQHLCGSHIVEALYLVCGERGFFYTFKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New chimeric proteins containing buman growth hormone fragment, used particularly for the production of human insulin
                                                                                                                            DNA encoding human insulin procursors - which comprise B- and
A-chains linked via amino acid chain contg. i or more glycosylation
sites, for propo. of insulic in tungal delis
                                                                                                                                                                                                                                           and A represent B- and A chains of insulin respectively, and Pg represents a modified C-peptide or any number of amino acids comprising at least one glycosylation consensus site, can be inserted into expression vectors which in turn can be used to transform fungal host cells. The fungal cells are then cultured and the insulin expressed in such cells can be harvested.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin: precursor; growth hormone; chaperone; intramolecular;
                                                                                                                                                                                                                             sequences encoding insulin precursors of formula H-Pg-A.
                                                                                                                                                                                                                                                                                                                                                                                                Length 86;
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                                               Van DEN HONDEL CAMJJ:
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100.0%; Pred. No. 8.4e-43;
iive 0; Mismatches 0;
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                                               Valinger R,
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(MESTZ) MESTRIC S.
(PLIV.) PLIVA PHARM & CHEM FAB
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N-PSDB; AAT17830, AAT17831
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                                             Punt PJ,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           The inventors claim a method for the prepat of an insulin priority in which the A-chain and 5-chain are joined through a connecting peotide. The connecting peptide joins the A-chain at the mained group of A-1 to the B-chain at the carboxyl group of B-30. The method is pref. for the prepat of human insulin precursor (see AAP46029). The SOS of the connecting peptides of a number of species are given (see AAP40023 to correct PA field.)
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                                                                                                                                                                                                                                                             Insulin precursor produ. from linear S-sulphonate and mercaptan in single step without separate ox(dn)_{\rm c}
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                                                                                                              800S-0134489.
800S-0210696.
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27-MAR-1980;
28-NOV-1980;
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Drecursor can be a component of chimeric proteins which additionally contains an Atenniana Insagnant of human growth hormone (Mai) and a cleavable peptide linker (AAVA285). The home provide humans a cleavable peptide linker (AAVA285). The home provide chimeric protein acts as an intramclecular chaperone (1MC) for the insular protein acts as an intramclecular chaperone (1MC) for the insular chaperone (1MC) for the insular chaperone (1MC) for the insular chaperone for the characteristic enabling it to fold correctly. The eleavable peptide linker confinent chaperone for the characteristic enabling it to fold correctly. The home protein of the characteristic enabling it to fold correctly. The degree of the fewer necessary procedural steps, and hence resulting in a higher yield of the fusion protein and decrease the intermolecular insular degradation by a microcialar the solubility of the fusion proteins and decrease the intermolecular interactions among the fission proteins, thus allowing folding of the fused insulin precursor at commercially useful high concentrations. The procedural steps of cyanadem bromide claesage, oxidative subhite systs and related contrations and evidence or validative subhite systs and related purification steps can thus be eliminated valor with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
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INTERP-3: antidiabetic: neuroprotective; anorectic; trangilliser:

Vulnerary; anorectic; cardiant; nepirotropic; dermactodicipiliser:

Vulnerary; anorectic; cardiant; nepirotropic; dermactological; antiHIV)

antiviral; hyperglycaemia; obesity; lung disease; glomerulonepiritis;
interstital nepirotropic; syndrome; syndrome; short stature; increased fat mass-to-lean ratio; immunological disorder:

peripheral neuropathy; multiple sclerosis; muscular dystrophy;

partabolic state; trauma; wounding; infection; HIV; skin disorder;

human immunodeficiency virus; diabetes; heart dystunction;

kidney disorder; whole body growth disorder.
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Pred, No. 8.4e 43;
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100.0%;
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Best Local Similarity
Matches 86: Conserv
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WPI: 2000-465955/40.

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The present invention describes an insulin-like growth factor (IGF)-1

24, 25, 43, 49 or 53, optionally in combination with an amino acid at

24, 25, 43, 49 or 53, optionally in combination with an amino acid at

position 12 and/or 16 of the native human IGF-1 sequence, is replaced

with an alanine, glycine, or a serine residue. The residue at position 7

may be rep, aced by any amino acid. (I) can have antidabetic, cardiant,

neuroprotective, anometic, tranquilliser, vubnerary, anometic,

nephrotropic, dermatological, antiHIV and antiviral activities. The IGF-1

mutants are used in any methods where IGFs or insulin are used, e.g. in

treating hypergycaemia, obesity-related, neurological, cardiac, renal,

munnological, and anabolic disorders. These disorders include lung

diseases, diometulomephritis, interstital nephritis. Turner's syndrome,

laron's syndrome, short stature, increased fat mass-to-lean ratios,

nmunnological disorders, peripheral neuropathy, multiple sclerosis,

muscular dysturchy, catabolic states, tranma, wounding, lifection,

human immunodeficiency virus (HVV), wounds, skin disorders, diabetes,

hart dysfunctions, kidney disorders, and whole body growth disorders.

They can also be used for increasing serum and tissue levels of

the libitation and insulin a mammal. The IGF-1 mutants improve the

halt-lives of IGF-1 and insulin. Sequence represents the

native furman proinsulin protein sequence, which is given in the
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                             Novel insulin-like growth factor (IGF) I mutants that selectively bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVICENTIA CONTROLLA IN TRANSPORTATION OF THE STATE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FVNQHLCCSHLVEALYLVCSBRGFFYTPKTRREAEDLQVGQVELGCCGPGAGSLQPLALEG
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                                                              to IGF binding protein (IGFBP)-1 or IGFBP-3, used to improve the half-lives of IGF-I and insulin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 86;
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100.0%; Pred. No. 8.4e-43;
dive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention.
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                                                                                                                                                                         Disclosure: Page 44; 48pp; English.
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100.0%; Fix
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86; Conservative
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Nest Local &
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AAM48219
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Ö <u>ن</u> 61

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1 FVNGHLGSSHLVBALYIVGSERGFFYIPKTRRBAEDLØVGOVERGGGPGAGSLOPLALEG
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                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protecting bacteria from phage injection - by transformation with aloning vector confg. segment with restriction and modification
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                                                                                                                                                                     Length 87:
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                  100.0%; Score 463; DB 3;
100.0%; Pred. No. 8.5e-43;
tive 0; Mismatches 0;
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                           The sequence comprises human proinsulin. (Cpdated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                  61 SLOKROIVEOCCISICSLYOLENYCN 86
11111 1111 11111 111111 1
62 SLOKRGIVEQCCISICSLYOLENYCN 87
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'label- B-chain
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/label= C-chain
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                                                                                                                                                                                                    Similarity
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                                                                                                              87 AA;
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                                                                                                                                                                                                                                                                                                         disorders. The method comprises contacting cutilidate with an artifly seen such as insulin like growth factor (16F-1) and/or with a kinding artifly preference for 10FBF 1, an LEF and owith a binding protein-7 (16FBF) 40 for 10FBF 1, an LEF and owith a binding affining preference for 16FBF 1 over 16BBF 3, or a 10FBF displacer peptide that prevents the interaction of 16FBF 40 and done not bind to human 16F receptor. The method is useful for treating cartillage disorders (CD) including degenerative CD, articular CD such as rheumatoid arthritis and obscourthoils. The present sequence is human profisult, which was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FVNORLGGSRLVBALXIVGGERGFFYFPKTRREABDLØVGQVFLGGGDPGAGELGPLALEG F.: (1111) + 111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1111) + 1111; (1
                                                                                                              degenerative cartilagenous disorders, by conjunting cartilage with insulia-like growth factor analog with altered affining for JOP-Finelia
                                                                                  Treating cartilage disorders including cartilage damage by injust
                                                                                                                                                                                                                                                                                       The present invention relates to a sethed for treating cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :5
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100.3%; Score 463; DB 23; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.4e-43;
Matches 86; Consorvative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SLOKRGIVEQCCISICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLOKEGIVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                         Disclosure: Fig 16: 136pp: English.
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82US 0354287.
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(first entry)
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                     WP1; 2002-382942/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human proinsulls
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-1981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP20036;
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                                                                                                                                                                     proteins
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AAP20035
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interferon and human tissue plasminogen activator. (Updated on 16-AGG-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
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85US-0697090.
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(updated)
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                                                       Coury Match
Best Local Similarity 100.0
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                         Synthetic proinsulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 1985-265030/43.
                                        87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAN50082
                                                                                                                                                                                                                                                                                                                                 Home sapiens
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31-JAN-1985;
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16-AUG-2002
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                                         Sednence
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                                                                   1 FVNOHLOGSHIVEALYEVCGERGFFYTPKTRREAEDLOVGOVELGGGPGAGSLQPMALEG 60
                                                                              autonomously replicating recombinant DNA expression vectors which comprise 1) a transcriptional and translational activating sequence which is in the reading frame of a nucleotide sequence which codes for a peptide or polypeptide; 2) a translational stop signal; 5) a translational start signal which is in the reading frame of a nucleotide sequence that codes for a functional polypeptide, on additional translational stop signal; The peptide; and 4) an additional translational stop signal; The peptide or polypeptide coding sequence codes for 2-20 AAs, esp. AAPS0122-PS0125. The functional polypeptide is esp. growth becomes, human translation.
                                                  Saps
                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA expression vector \cdot with autonomous replication and on transcription generating polycistronic mrna
                             Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim a process for preparing selectable and
                                                 Indels
                                                                                                                                                                                                                                                                              Selectable vector; autocombusly replicating sector;
                     Sequence of the 32 Noterminal AAs of proinstiin.
                                                                                                                     SLOKEGIVEQCOTSICSLYQLENYCN 87
                                                                                                           SLOKRGIVEGCCTSICSLYQLENYCN 86
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/label- B chain
67..87
/label= A chain
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85CN-0101555,
                                                                                                                                                                                                                                         (first entry)
                                                 86; Conservative
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                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       expression vector
          87 AA;
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                                                                                                                                                                                                                                                                                                            Homo sapiens.
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30-SEP-1991
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                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                           51
          Sequence
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Region
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AAP50127
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                                                                                                                                              2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDI,OVGQVELGGGPGAGSLQPLALEG
                                                                                                                 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in producing proteinaceous granules in cell transformants, esp
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The synthetic proinsulin gene is expressed in a new selectable and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New selectable and autonomously replicating DNA expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autonomously replicating recombinant DNA expression vector comprising a runaway replicon and a transcriptional and translational activating sequence in the reading frame of the proinsulin coding sequence, the sequence confg a translational stop signal. Host colls confg, the vector, which is esp. plasmid pC2103, are cultured, and proinsulin is produced as a highly homogeneous species of proteinaceous granule. The granule can be
                                                           0;
Length 87;
                                                           Indels
                                                           .
O
; Score 463; DB 6;
; Pred. No. 8.5e-43;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector; proteinaceous granule;
                                                                                                                                                                                                                                  61 SLQKRGIVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                            52 SLOKRGIVEOCCTSICSLYOLENYCN 87
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/label-C chair.
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61 SLOKRGIVEGCTSICSLYQLENYCN 86
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86; Conserv
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18 - JUN - 1993
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                                                                                                                                                                                                                                                                                                                                                                                             1 PVNOHIGGSHIAPALYLVGGENGFPYTPKTREHARDL, VAOVELGGEFTAGSLETT (111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 - 1111 -
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readily isolated from cell lysates and is stable on washing with urea or detergent spins, at low opens, The grant, contains at least 50% of probabilization and isolation operations are simplified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant plasmid; E.goli expression vector; secretion vector
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                                                                                                                     (Updated on 16-AUG-2002 to add missing os field.)
(Updated on 25-MAR-2003 to correct PA field.)
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810S-0222010.
810S-0286076.
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hes 85; Conservative
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Matches 86: Conserv
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02-JAN-1981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this sequence represents human proinsulin and was decoded from the sequences given in AAQ36996-7001. The CDNA fragment coding for proinsulin was inserted into plasmid vector profit and digested with KPLI and HindIII. This resulted in the formation of the vector pPLNS A trayment encoding amino acids 1-73 of CAT (see AAQ37002) was inserted into pPLNS to give a plasmid which contained DNA sequences which coded for amino acids 1-73 of CAT, an 8 amino acid linker sequence and human proinsulin. This plasmid, pUC-CAT-proinsulin, could be used in the formation of insulin analogues which may be used in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FVNOHILGGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG
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Insulin analogue; type 1; type 1; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selective and peripheral selective human insulin and their corresp. DNA, for treatment of type I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 463; DB 14; Length 87; 100.0%; Pred. No. 8.5e-43;
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AAR32367 standard: Protein; 87
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                                                                                                                                                                                                                    Proinsulin protein sequence.
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92US-0918953.
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(first entry)
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WPI: 1993-102806/13.
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Bost Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                               N-PSDB; AA038310.
                                                                                                                                                                                                      22-SEP-1992;
                                                                                                                                                                                                                          24-SEP-1991;
                                                                                                                                            Homo sapiens
                                                                                                                                                                                   31-MAR-1993.
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21-APR-1932
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19-JUL-1993
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                                         AAR33855;
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         AAR33855
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3 FVNQHLGGSHLVEALYLVGGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This modified human insulin precursor comprises an Noterinal initiating dipeptide, chosen from MetTyr or MetAty, which does not define a cathepsin C dipeptide removal stup point. This dipeptide is linked to the natural human insulin before its connection peptide and natural human insulin Administration of Dipeptide removal is carefully controlled to obtain the desired prod. Without further degradion occurring, irrespective of whether the next dipeptide in the sequence defines a cathepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
                                                                                                                                                                                                                                                                                                                                                                                                                       or Metarg initiating
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                                                                                                                                                                                                                           numan
                                                                                                                                                                                   /label-N-terminal initiating dipeptide
                                                                                                                                                                                                            /label-natural connecting populde of proinsulin
                                                                                                                                                                                                                                                                                                                                                                               McDonough JP:
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                                                                                                                                                                                                                                                       /label-native human insulin A-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human insulin precursor - contg. Met-Tyr or MeT-a
dispeptide for controlled removal by cathepsin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLOKRGIVEQCCTSICSLYQLENYCN 86
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                                                                                                                                                                                                                                                                                                                                                                             Mackellar WC,
                                                                                                                       Ruman insulin precursor; exthepsin C.
                                                                                                                                                               Location/0.allfiers
                   AAR07682 standard: protein; 88 AA.
                                                                                                  Modified human insulim precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, page 3, 8pp, English.
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                                                                                                                                                                                                                                                                                                                   9055-0304890,
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                                                                              (first entry)
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                                                                    09-JAN-2003
13-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                               Becker GW,
                                       AARC7682;
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RESULT 12
          AAR07682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents an analogue of native human proinsulin (hpI). The SMA encoding this sequence was used in the construction of the expression vector of the invention. The coding region of the hpI gene was synthesised and was cloned into the expression plasmid pCZRIZ6S (see also AAQ38307). Expression of this gene lead to the inclusion of an extra amino acid (Arg) in the second position from the N-terminal of mature hpI. The extra amino acid provides increased expression levels of the protein and is then cleaved off to avoid undesirable (updated on 25-MAH-200) to correct PN field.)
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                                                                                                                                                                                                                                                                     Proinsulin; hpI; native; pCZR126S; expression vector; E. ccli; human; expression; immunological effect.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of low molecular wt. polypeptide(s) e.g. insulin growth factor I · by expressing as deriv. with N-terminal amino acid to provide increased expression levels
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AAR33855 standard; Frotein; 88 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The fusion product is encoded by a synthetic sequence having at its 5'-end a medification of the 3'-end or the naturally occurring alpha-factor secretory leader and processing signal sequence, where three G.u.Aia pairs have been deleted. A plasmid containing the synthetic proinsulin coding sequence was used to transform kex2-mutant yeast strains in the presence or absence of the closed KEX2-ques. Post-translational processing of pro-insulin into peptides only occurred in yeast transformed to KEX2 plus, see also AA220545. (Opdated on 25-MAR-2003 to correct PA field.)
                                                                  BCA-5; yeast preferred codons; postitranslational procession; insulin; endopeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%, Score 463; DB 13; Longth 92; 100.0%, Pred; No. 9e-43; ive 0; Mismatches 0; Indels
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Yeast alpha-factor signal-buman proinsulis fusion product
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Matches 86: Conservative
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                                                                                                                                                                                                                                                                        Cleavage-site
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08-APR-1988;
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                                                                                                                                                                       Syntheric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The proinsulin is expressed in Saccharomyces cerevisiae A3103.1. It is encoded by a synthetic gene (see AAN90279). The 3 consecutive peptides are proinsulin chains B, C and A resp. The regions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression and secretion of heterologous proteins in yeast - using truncated a factor leader sequence contg. signal peptide and slycosylation site.
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                                                                                "dibasic processing site"
                                                                                                                                                                   "dibasic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dibasic processing sites. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                   /note= "dibasic processing s
73...93
/note= "proinsulin chain A"
                                         "proinsulin chain B"
                                                                                                                          "proinsulin chain C"
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Job time : 61.4158 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; fig 1: 22pp: English.
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                                                          38..39
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38..72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN90279
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                                                                                                                                                                                                                                                                                                                                   23-DEC-1988;
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GenCore version 5.1.6 Capyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

September 15, 2003, 11:57:40 : Search time 19.7276 Scoonds (without alignments) 184:449 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

1 FUNQHICGSHLVEALYLVCG........VEGCCTS:CSLYQJENYCN 86 US-09-423-100-4 463

BLOSUM62 Gapop 10.0 . Gapext, 0.5 Scoring table:

328717 segs, 42410858 residues Searched: ,28717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20090030000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /egn2_6/ptodata/l/laa/5A_DCMB.pcp.*
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5: /egn2_6/ptodata/l/laa/FB_DCMB.pcp.*
6: /egn2_6/ptodata/l/laa/FCJUS_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printer, and is derived by analysis of the total acore distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	80	Ω	101 (0) (1084)
	463	100.0	86	-	US-09-477-924-2	Sequence 2. And 1
7	463	100.0	98	~•	-09-723	· ::
3	463	100.0	986	₹	US-09-723-896-2	7
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S	463	100.0	96	7	-60-	-
9	463	100.0	96	₹	US-09-386-303A-4	÷
۲۰.	463	150.0	97	-		Sequence 4, Aprli
80	463	100.0	110	٣,	US-08-950-720A-11	: •
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10	463	100.0	077	~	US-08-784-582-2	લ
11	463	100.0	110	~	US-08-785-271-2	Sequence 2. Appl:
12	463	100.0	110	÷	US-08-472-701-2	2
13	463	100.0		4	US-09-185-852-2	7
14	463	100.0		S	PCT-US95-08596-2	2, 4
15	463	100.0		₹	JS-09-280-030-63	9.9
16	463	100.0	130	4	US-08-280-030-62	62.
17	463	100.0	1.5	~	US-08-508-664-15	Š
60 F1	463	100.0	_	7	US-08-508-664-16	9.1
19	463	100.0	16	-	US-07-918-953-8	8,
20	463	100.0	167	-	081-561-	œ
21	457	98.7	2	(7		٠,
22	457	98.7		-3*	US-09-386-303A-5	Sequence 5, Appl:
23	457	98.7		~	US-08-369-487-7	Sequence 7. Appli
24	456	98.5	06	-	US-08-030-731A-43	Sequence 43. Appl
25	446	66.3	97	~	307	Sequence 6, Appl:
58	444	6.55	97	~	US-09-099-307-8	Sequence 8, Appl:
27	443	95.7	110	m	US-08-589-028-4	Sequence 4. Appli

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Sequence 4	Sequence 4	Sequence 7	Sequence 1	Seguence 7	Seguence 1	Sequence 3	Sequence 6	Sequence 1	Sequence 2	Sequence 8	Sequence 5	Sequence 7	Sequence 4	Sequence 1	Sequence 9	Sequence 4	Sequence 4
US-08-784-582-4	US-08-785-27:-4	US-09-095-307-7	US-09-095-307-11	US-09-676-787-7	US-08-531-986A-1	US-08-981-988A-3	US-08-981-988A-6	US-09-484-848-16	US-08-981-988A-2	US-08-981-988A-8	US-06-981-968A-5	US-08-981-988A-7	US-09-201-227A-43	US-09-484-848-15	US-06-981-968A-9	US-08-981-988A-4	US-08-233-617-4
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95.7	95.7	95.0	94.5	86.0	63.2	62.7	62.3	62.3	67.9	61.7	61.4	60.8	60.7	60.5	60.4	60.2	58.9
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AL IGNMENTS

Sequence 2. Application US/09477924
Patent No. 5463764
GENERAL INFORMATION:
APPLICANT: Dubaquie, Yves
TITLE 0F INVENTION: PROTEIN VARIANTS
TITLE OF INVENTION: PROTEIN VARIANTS
TITLE REPERENCE: P17.281-1
CURRENT APPLICATION NUMBER: US/09/477,924
CURRENT FILMS CATE: 2000-01-05
NUMBER OF SEQ ID NOS: 6 DEGANISM: Homo sapiens US-09-477-924-2 18-09-477-924-2 SEQ ID NO 2 LENGTH: 86 FR FR

90 : FVNQHLCGSHLVEALYLYCGSRGFFYTPKTRREADHJOVGOVELGGGPGAGSLQPLALEG 60 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGFGAGSLQPLALEG Gaps ö Obery Match 100.0%; Score 463; DB 4; Length 86; sest Local Similarity 100.0%; Pred. No. 1.5e-47; Matches 66; Conservative 0; Mismatches 0; Indels 61 SIQKRGIVEQCCTSICSLYQLENYCN 86 61 SLOKRGIVEGCCTSICSLYQLENYCN 86 3 2 5 õ

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US-39-73-981-2
Sequence 2. Application US/09723981
Sequence 2. Application US/09723981
Sequence 2. Application US/09723981
Sequence 2. Application US/09723981
Sequence 3. Application Underly
TILLE OF INVENTION: PRCTEIN VARIANTS
FILE REFERENCE: PILLNS
CCRRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/723,981
CCRRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/477,923
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 2
LENGTH: 86
LENGTH: 86 TYPE: PRT OKGANISM: Homo sapiens US-09-723-981-2 us-09-423-100-4.rai

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Gaps

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0; Indels

Mismatches

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86; Conservative
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) LOCATION:
US-09-134-836-4
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| Patent No. 653428.
| GENERAL INFORMATION:
| APPLICANT: FUSITEDIO Inc.
| APPLICANT: KURANO, Yeshihiro
| APPLICANT: KURANO, Yeshihiro
| APPLICANT: NISHIZONO, Isac
| APPLICANT: NISHIZONO, Isac
| TITLE OF INVENTION: Immuneassay For Neasuring Human C-Peptidm and R:: Incertor
| FILE REFERENCE: 0760-0291P
| CURRENT APPLICATION NUMBER: US/09/878, 980
| CURRENT FILING DAIE: 2001-06-12
| PRION FILING DAIE: 2000-05-12
| PRION FILING DAIE: 2000-05-12
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: Patentin version 3.
                                                                                        1 FVNQHLCGSHLVEALYLVCGBRGFFYTFKTRÆRALDLCVGVVSLGGGRAGSLGFLALDE ED
                                                                                                            1 FVNGHLGGSHLVEALYLVGGERGFFYTPKTRREAEDLGVGGVELGGGRGAGSLQPLALEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FVNQHLCGSHLVEASYLVGGERGFFYTPKTRREAEDLQVSQVELGGGPGAGSLQPCALEG 60
               Score 463: PM 4: Tength 86;
Pred. No. 1.50-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 463; DR 1; Length 86:
Pred. No. 1.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                      C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 463; DB 4;
106.0%; Pred. No. 1.5e-47;
ive 0; Mismatches 0;
                                                    C; Mismatches
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dubagaite, Yves
APPLICANT: Dubagaite, Yves
TITLE OF INVENTION PROTEIN VARIANTS
FILE REPERENCE: P1712R
CURRENT APPLICATION NUMBER: US/CU/723,896
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/C9/477-923
NUMBER OF SEQ ID NOS: 6
                 100.0%; Score 463;
                                                                                                                                                            61 SLOKKGIVEQCCTSTCSLYULENYON 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SLQKRGIVECCTS1CSLYQLENYCN 86
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                                                                                                                                                                                                                                                                                      // Sequence 2, Application US/09723896
// Patent No. 6509443
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                                  100.0%;
                                                    86; Conservative
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-878-383-1
                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                               ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                       RESULT 3
US-09-723-896-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-723-896-2
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US-C9-878-380-1
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LENGTH: 85
                 Query Match
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APPLICANT: Rubroder, Franz-Josef
AFPLICANT: Keller, Reinhold
TITLE DF INVENTION: improved process for obtaining
TITLE DF INVENTION: insulin precursors having correctly bonded cystine bridge
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                          1 FVNQHLCGSHLVEALYLVGGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Finnegar, Henderson, Farrabow, Garrett & ADDRESSE: Dunner STREET: 1302 [ Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCFTWARE: Patentin Release #1.0, Version #1.30 CURRENI APPLICATION DATA: PPLICATION NUMBER: US/09/134,836 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCRNEY/AGENT INFORMATION:
NAME: Lesite McDonell
REGISTRAILON NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481.1600-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                   61 SLOKKGIVEGODSTSLOSINGLENYCN 86
-11111:1 1111 1111 1111
61 SLGKRGIVEGODSTSLOSINGLENYON 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERAIING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          TS-09-134-836-4
Sequence 4, Application US/09134836
Datem No. 598648
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 408-406
TELEFAX: (202) 408-4406
INFORMATION FOR SEQ 1D NO: 4
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LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86; Conservative
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1..96
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1 PVNCHLOSSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Overy Match 100.0%; Score 463: DB i: Length 97; Best Local Similarity 100.0%; Pred. No. 1.8e-47; Matches 86; Conservative 0; Mismatches 0; Indels
      Process For Obtaining Proinsulin
                                                                                                                                                                                                                                                                                                                              ZIP: 08876-1258
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 386
COMPUTER: IBM 386
TITLE OF INVENTION: Process For Obtaining Proinsul
TITLE OF INVENTION: Possessing Correctly Linked
TITLE OF INVENTION: Cysting Bridges
NUMBES OF SECUENCES: 7
CORRESPONDENCE ADDRESS:
ACDRESSES Remeth A. Genoni, Esq.
STREET: Rt. 202-206 No. $473049th/P.O. Box 2500
CITY: Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Barbara V. Maurer, Esq.
FEGISTATION UNBER: 31,287
REFERENCE/DOCKET NUBER: HOE 92/F 384
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPURFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,376A
FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER: GF 4240420.7
FILING DATE: December 2, 1992
ATICKNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CONKlin, Darrell C.
APPLICANT: LOTtom-Day, Catherine E.
APPLICANT: LOK, SI
APPLICANT: Jaspers, Slephen R.
IITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TITE THE TOTAL STORY S
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STREET: 1201 Eastlake Avenue Bast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS-08-950-720A-11
Sequence 11, Application US/08950720A
Factors No. 6046028
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IELEPRONE: (908) 231-4079
TELEFAX: (908) 231-2255
INCOMMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGIH: 97 Amino Acids
TYPE: Amino Acid (AA)
                                                                                                                                                                                                                                                                             New Jersey
: U.S.A.
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STREET: 120-
TTY: Seattle
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                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                      CITY: S
STATE:
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             US-UN-190-1904

Sequence 4. Application US/09:86303A

; Sequence 4. Application US/09:86303A

; Patent No. 638035

; GENERAL INFORMATION: Fyany-Josef

APPLICANT: Relicr. Reirhold

; TITLE OF INVENTION: Ingroved process for octaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FVNQHICGSHLVBALYLVGGERGFFYTPKTRRFAEDLQVGOVELGGGPGASSLQPLALER 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 FVNQHLGGSBLUVFALYLV/GERGFFYTPKTRRFAEDLQVGQVELGGGGGAGSLGFLALES 30
                                                                                                                                                                                                                                                                  NUMBER DF SEOUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrahow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sength 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIOM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version: #1.30
CURRNI APPLICATION DATA:
APPLICATION NUMBER: US/09/386.303A
FILING DATE: 31-A:q-1999
CLASSIFICATION: <UNKNOWN:
APPLICATION: <UNKNOWN:
FILING DATE: <UNKNOWN:
FILING DATE: <UNKNOWN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Leasile McConcel.
REGISCRATION NIMBER: 34,872
REFERSINGE/DOCKET NUMBER: 02481.1600-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOMATION: 1.196
SEQUENCE DESCRIPTION: SEGIE NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLOKRGIVEQCCTSICSLIGHT::||
SLOKRGIVEQCCTSICSLIQLENYCN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SLOKAGIVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPRIONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACIENTSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08150376A
Patent No. 5473049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 96 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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Gerl, Martin
Ludwig, Jurgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALDHLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                               Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
SIATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sabel, Walter
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                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300
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Best Local Similarity
Matches 86: Conservat
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APPLICANT: Oberme
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APPLICANT:
APPLICANT:
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US-08-160-376A-4
      US-09-386-303A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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Length 110;
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pate::In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      Chery Match 190.0%: Score 463; DB 3;
Rost Local Similarity 100.0%: Pred. No. 2.1e-47;
Matches 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/06/784,562
FILING DATE: Concurrently Herewith
CLASSIPICATION: 435
PHORA APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-OCT-1996
PRICH PAPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Halban, Fhilippe A.
No. 6110797mington, Karl D.
Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRET: P.C. Box 4433
SIRIT: Houston
STATE: Houston
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REFERENCE/DOCKET NUMBER: UTSD:514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Newgard, Christopher B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Segmence 2, Application US/08784582
Fatent No. 6110767
GENBRAL INFORMATION:
  TELEFAX: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECCMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                          linear
                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                          TOPOLOGY:
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TYPE: am
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APPLICANT:
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APPLICANT:
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APPLICANT: Haiban, Philippe
APPLICANT: Haiban, Philippe
APPLICANT: No. 688729minqton, Karl D.
APPLICANT: Clark, Samela A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Tringen, Anice E.
APPLICANT: Rise, Fred
TITLE OF INVENTION: Recombinant Expression of Proteins From TITLE OF INVENTION: Scoretory Cell Lines
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 463; DB v; Longth 110:
100.0%; Pred. No. 2.1e-47:
tive 0: Mismatches 0: Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version 41.36
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: H.ghlander, Steven :
REGISTRATION NUMBER: 47,642
REFERENCE/DOCKET NUMBER: UTSD:426\HYL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STOKKGIVEQCCTSICSLYOLENYON 110
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FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                    APPLICATION NUMBER: US/03/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnoid, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-589-028-2; Sequence 2, Application US/085;9628; Patent No. 6087129
                                                                                                                                                                        NAME: Sawislak, Deborah A
REGISTRAIION NUMBER: 37,438
REFRENDZ/DOCKET NYMBER: 96-0'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPHAN: 206-442-6673
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 13:
SEGUENCE CHARACTER(STICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: No. 66460286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
21P: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 86: Conservative
CURRENT APPLICATION DATA
                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                FILING DATE:
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Gaps
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APPLICANT: Owande, Christian:
APPLICANT: Kruse, Fred
APPLICANT: Kruse, Fred
APPLICANT: WGarry, Dennis
TITLE OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
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1 FVNQHLGGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Osborne, William R.A. APPLICANT: Ramesh, Nagarajan FILE OF INVENTION: Compositions and Methods for Treating Diabetes PILE REFERENCE: P-UW 3264 CURRENT APPLICATION NUMBER: US/09/185,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 463; DB 4; Length 110; 100.0%; Pred. No. 2.1e-47; .ive 0; Mismatches 0; Indeis 0
                                                                                                                                                                                                  APPLICANT: Griffin, An: C.
APPLICANT: Hickey, William F.
IIIE OF WHATON: Detection and Treatment Methods for IIIE OF INVENTION: Type I Diabetes
NUMBER OF SEQUENCES: 23
CORRESPONDENCE S: COCKFIELD
ADDRESSE: LAHIVE S COCKFIELD
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                     51 SLOKRGIVEQCCTSICSLYQLENYCN 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCHI Text
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31.503
REFERENCE/DOCKET NUMBER: DCI-092DV
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             E: LAHIVE & COCKFIELD 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/272,223
FILING DATE: 08-7JLY-1994
CLASSIFICATION: 435
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Patent No. 6537806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
                                                                                                                                          Sequence 2, Application US/08472701
Patent No. 6509165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FCR SEQ 1D NO: 2
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hest Local Similarity 100.
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                 02109-1875
                                                                                                                                                                                     GENERAL INFORMATION:
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STATE: MA
COUNTRY:
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                                                                                                     PESULT 12
US-08-472-701-2
                                                                                                                                                                                                                                                                                                                                                     SIREET:
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                                                                                                                                                                  25 FVNQHLGGSHIVEALYIVCGSRGFFYIFKTSRBAEDLGVQCVBEGGGFGAGSHQFLALES 84
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                                                            Dength 110;
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CURRENT APPLICATION DATA:
                                                          ch 190.0%; Score 46%; DB %; DB Bl Similarity 100.0%; Pred. No. 2.1e-47%; 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KINSE, Fred
TITLE OF INVENTION: RECOMINANT EXPRESSI:
TITLE OF INVENTION: SECRETORY CELL. LINES
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  Newgard, Christopher B.
Halban, Philippe A.
No. 6194176mington, Karl D.
                                                                                                                                                                                                                            61 SLOKRGIVEQCCTSICSLYOLENYON 86
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FILING DATE: Concurrently Relewit:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Highlander, Steven L.
REGISTATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:513
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/419-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION LATA:
PREDICATION NUMBER: US 08/589.028
PRICK DATE: 19-4AN-1996
ATIOHNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08785271; Patent No. 6194176
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COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark, Samuel A.
Thigpen, Anice E.
Quaade, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 86; Conserv
TOPOLOGY: linear
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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US-08-784-582-2
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TITLE OF INVENTION: and Treatley Type I Blabetes
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 463; 38 4; Length 110; 100.0%; Pred. No. 2.16-47;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-PCS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/38596
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NAME: DeCont.; Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REPERENCE/DOCKET NUMBER: DC1-052PC
TELECOMMUNICATION: INFORMATION:
TELECHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: LAHIVE & COCKTIELD
STREET: 60 State Street, suito 510
CURRENT FILLING DAIE: 1998-11-64
EARLIER APPLICATION NUMBER: 60/087,660
EARLIER FILLING DAIE: 1998-56-02
SOFIWBER OF SEO ID NOS: 1:
SOFIWARE: Patentin Ver: 2:0
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INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTER:STICS:
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APPLICATION NUMBER: US GR
FILING DATE: 08-JULY-199:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     il0 arino acids
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Best Local Similarity 160.
Matches 86; Conservative
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Best Local Similarity 160.8
Matches 86; Conservative
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COUNTRY: USA
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CLASSIFICATION:
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PCT-US95-08596-2
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LENGTH: 110
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APPLICANT: Saco, Soiji
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APPLICANT: Saco, Soiji
APPLICANT: Hqgash:Rusii, Nachiko
APPLICANT: Kondo, Masaaki
TITLE OF INVENTION: DREPARING JSEVUL POLYPEPTIDES THROUGH EXPRESSION OF THE
TITLE OF INVENTION: DRABBER: US/39/280,630A
TITLE OF INVENTION: DRABBER: US/39/280,630A
TITLE OF INVENTION: DRABBER: US/39/280,630A
CHEREN PPLICATION NUMBER: US/39/280,630A
CHEREN PPLICATION NUMBER: US/39/280,630A
SACULER APPLICATION NUMBER: US/39/280,630A
NUMBER: OF SEC ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 63
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Matches 86: Conservative
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us-09-423-100-4.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2663 Compugen 15d.
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OM protein · protein search, using sw model

September 15, 2003, 12:03:35 ; Search time 36.0645 Seconds (without allgoments) 347:945 Million cell updates/sor Run on:

US-09-423-100-4

Perfect score:

463 1 FVNQHLGGSHLVFALYLVGG......TVFDGCTSICSLYQLENTON 96 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

541936 seqs, 145912426 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000600000

Post-processing: Minimum Match 0% Maximum Match 100% Listing lirst 45 summaries

Database :

/cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

/ogn2_6/ptodata/1/pubpaa/JS1.C_PTBCOMB_pop: /con2_6/ptodata/1/pubpaa/JS1.C_NEW_PUB_pop:* /con2_6/ptodata/1/pubpaa/JS66_NEW_PUB_pop:* /cgm2_6/ptodata/1/pubpaa/US50_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to here a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTER

Descript (c.:			Sectionce 4. Appli	Sequence 2, Applia		Sequence 4 Appli	. 15	Sequence 3 Appli	Secure C economic		Sequence 1. Appli					
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it: DB	- C - 36		1.	85 14	86 14	96 10	10 9	6 011	10 10	10 12	10 15	110 15	17 9	90.08	95 10	166 9
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- CANGRALING PRINTING APPLICANT: FUJICEDIO INC.
- APPLICANT: KUTAJIMA, Sachiko
- APPLICANT: KUTAJIMA, Sachiko
- APPLICANT: KUTAJIMA, Sachiko
- APPLICANT: KUTAJIMA, VOSLIhiro
- APPLICANT: KUTANO, YOSLIhiro
- APPLICANT: KUTAJIMA, FOSLIHIRO
- ISTIE DE INVENTION: Immunoassay For Measuring Human C-Peptide and Kit Therefor
- FILE REFERENCE: C760-0291P
- CURRENT FILLING DATE: 2001-06-12
- FILE REPERIORATION NUMBER: UP 2000-174691
- FILLING DATE: 2000-06-12
- NUMREK :P SRD IS NOS: 2
- SOTTOM FILLING DATE: 2000-06-12
- NUMREK :P SRD IS NOS: 2
- SOTTOM FILLING DATE: 2001-06-12
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100.0%; Pred. No. 9.7e-45;
Live 0; Mismatches 0;
Conservative
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                                                                                                         WEMPLICANT: UNIVERSELY PROBLEMS APPLICANT: UNDAQUIO. YVES
APPLICANT: PILVAROIT, Ellen
APPLICANT: FILVAROIT, Ellen
APPLICANT: FILVAROIT, Ellen
ITTLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISCROERS
FILE REFERENCE: P1794R1
CURRENT APPLICATION NUMBER: US/09/888,335R
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/248,985
PRIOR APPLICATION NUMBER: US 60/204,450
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 153
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Publication No. US/2020160955A1
CENTRAL INFORMATION: APPLICANT: DUMBAN, PROPER ALTILE SET INVENTION: PROPER VALIE REFERENCE: P1712R1-1
CURRENT APPLICATION: PROPER VALIANTION: CURRENT APPLICATION NUMBER: US/10/028,4:0
CURRENT P111NG DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/477,924
PRIOR FILING DATE: 2000-01-3:
NUMBER OF SEO ID NOS: 6
SEO ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SLQKRGIVECCCTSICSLYQLENYCN 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLOKRGIVEOCCISICS: YQLENYCN 86
Sequence 4, Application US/098589358 Publication No. US2063066917741 GENERAL INFORMATION:
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100,0%;
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Matches 86; Conservative
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Best Local Similarity
Thes 86/ Conserva
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US-10-028-410-2
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APPLICAN., nuclear, relation.

Keilar, Relator, Relation.

ITLE OF INVENTION: Improved process for obtaining insulin precursors having correctly bonded cystine bri
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APPLICANT: Gan, Ziong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
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                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPUTER
COMPUTER: ISM PC COMPUTED
COMPUTER: ISM PC COMPUTED
COMPUTER: PALENTE RELEASE #1.6, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-Jan 2002
CLASSIFICATION: <a href="Computer">CURRENT DATE: CAPA 2002</a>
CLASSIFICATION: <a href="Computer">CURRENT DATE: CAPA 2002</a>
CLASSIFICATION: <a href="Computer">CURRENT DATE: CAPA 2002</a>
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                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: WO 09/423,100
FILING DATE: 11-DEC-2000
ATTORNEY/AGENT THYORMATION:
NAME: MYCTOFIL, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/POCKET NUMBER: 020167-500130US
INFORMATION FOR SEC 12 NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 463; DB 14;
100.0%; Pred. No. 9.7e-45;
ive 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
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GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 106.0
Warnes 86, Conservative
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STATE: D.C.
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Sequence 3, Application US/09815229
Fatent No. 3520020058614A1
GENERAL INFORMATION:
APPLICANT: Filvaroff, Ellen H.
APPLICANT: Okumu, Franklin W.
TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS FILE REFERENCE: P1786R1US
CURRENT APPLICATION NUMBER: US/09/815.229
CURRENT FILING DATE: 2001-03-22
FRICH APPLICATION NUMBER: US 60/192,103
FRICH FILING DATE: 2000-03-24
NUMBER OF SEO ID NOS: 17
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                      1 FVNORLOGSHLVEALYLVOGERGFFYTPKTRRBAEDLQVGQVELGGGPGAGSLQPLALEG 60
                                             25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG
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Sequence 9, Application US/09804409A
PATCH. No. US20020155100A1
GENERAL INFORMATION
APPLICANT: KIEFFER, TIMOTHY 3.
APPLICANT: CHEUNG, ANTHONY 7.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
TITLE OF INVENTION: EXPERSION IN GUT
FILE PERERNOE: 029996/027 872;
CURRENT APPLICATION NUMBER: US/09/804.409A
CURRENT APPLICATION NUMBER: US/09/804.409A
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTLE VET. 2.1
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Best Local Simi
Matches 86; /
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US-09-815-229-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 125. Application US/C9205658
patent No. US2C016029517a1
GENERAL INFORMATION:
APPLICANT: RUKKUN. GATY
APPLICANT: Ogc. SCOT.
TITLE OF INVENTION: IMPERABED GLUGGSE TOLERANDE CONTITIONS
FILE REFERENCE: OGC.
CURRENT ADPLICATION NUMBER: US/O9/205,658
CURRENT ADPLICATION NUMBER: US/O9/205,658
GRALER APPLICATION NUMBER: US/O9/205,658
EARLIER APPLICATION NUMBER: US/OS/205
EARLIER APPLICATION NUMBER: US/OS/205
EARLIER APPLICATION NUMBER: US/OS/205
EARLIER PICANG DATE: 1997-05-15
EARLIER PICANG DATE: 1998-05-15
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                    PatentIn Pelease #1.0, Version #1.30
                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 02481.1600-00606
TELECHMANDINCALTION INFORMATION:
TELEPLAS: (202) 4.08-4.00
TELEPAX: (202) 4.08-44.00
INFORMATION FOR SEV. 13.01.4
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Matches 85; Cosservative 0; Mismarcher 44;
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                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/347,563
FILING DATE: C7-Sep-2001
CLASSIFICATION: <Unknown>
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ 1D NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 SLOKRGIVEOCCISICSLYOLENICH 96
                                                                                                                                                                      FILING DATE: <U:known>
ATTORNEY/AGBNT INFORMATION:
NAME: Loslie NCO::01
REGISTRATION NUMBER: 34,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                 IYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-205-658-125
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LENGIH: 110
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                                    25 FVNQHIGGSHLVFALYLVGERGFFYIPKTRREABDLQVGQVELGGGGGGGGLGPLHHHH
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OSPOCHOR, William R.A.
APPLICANT: Ramesh, Nagarajan
ITILa FO LINGWANTO. Compositions and Methods for Treating Diabetes
FILE REPERENCE: P-UW 3262
CURRENT APPLICATION NUMBER: US/10/328,813
FUCRENT FILMS DATE: 2602-12-23
PRICK APPLICATION NUMBER: US/39/185,852
PRICK APPLICATION NUMBER: 05/39/185,852
PRICK APPLICATION NUMBER: 60/087,666
PRICK APPLICATION NUMBER: 60/087,666
PRICK APPLICATION NUMBER: 1998-06-02
PRICK APPLICATION NUMBER: 1998-06-02
PRICK APPLICATION NUMBER: 1998-06-02
PRICK APPLICATION NUMBER: 1998-06-02
PRICK FILMS DATE: 1998-06-02
PRICK APPLICATION NOS: 2:0
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                                                                                                         95 SLOKRGIVEOCCTSICSLYQLENYCN 110
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 106.
Matches 86, Conservative
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ORGANISM: Homo sapiens
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TS-10-328-813-2
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                                                                                        Sequence 6, Application US/59469248C

Publication No. US2033161859Ai

GENERAL INFORMATION:

APPLICANT: ARIZEE FHARMACEUTICALS, INC.

APPLICANT: SHERIDAR, PHILE, J.

APPLICANT: SHERIDAR, PHILE, J.

APPLICANT: SHERIDAR, PHILE, J.

APPLICANT: SHERIDAR, PHILE, J.

APPLICANT: GLYNN, Jacquolien, M.

FILE REFRENCE: 05722-033

CURRENT APPLICATION NUMBER: US 60/248, 919

PRIOR FILING DATE: 2009-11:-13

PRIOR FILING DATE: 2009-11:-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 463; DB 12; 100.0%; Pred. No. 1.3c-44;
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Publication No. US2003054546741
GENERAL INFORMATION:
APPLICATION Orban, Tihamer
TITLE OF INVENTION: AUTOANTISEN VACCINE
FILE REFERENCE: 10276-067061
CURRENT APPLICATION NUMBER: 105/10/036,686
CURRENT FILING DATE: 2002-05-31
PRIOR PILICATION NUMBER: 60/250,068
PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASLSEO LOT Windows Version 4.5
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SLOKRGIVEQCCTSICSLYQLENYCN 110
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Best Local Similarity 100.
Matches 86; Conservative
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Best Local Similarity 100.
Matches 86; Conservative
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ORGANISM: Home saptens
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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Falcatu No. US20520081659A1

CANEXAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodics
FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925.297

CURRENT APPLICATION NUMBER: PCT/US00/05989

PRIOR PILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989

PRIOR FILING DATE: 2006-03-08

PRIOR FILING DATE: 2006-03-08

PRIOR FILING DATE: 3006-03-08

NUMBER OF SEQ IO NOS: 929

SOFTWARE: Patentin Ver. 2.0
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COMPUTER REALGHEEFORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM FO COMPATIBLE
COMPUTER: LBM FO COMPATIBLE
CHEMATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURNENT APPLICATION DATA:
APPLICATION NUMBER: US/05/947,563
FILING DATE: O'-Sep-2001
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION CATA:

APPLICATION NUMBER: 09/134.836
FILMO ATE: 4.0AKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: LEASINE MCDORG1
REGISTERSING NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481.1600-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDHESS: Sligle
TCPOLOGY: linear
MCLECULE TYPE: protein
ORIGINAL SOURCE:
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SEQUENCE CHARACTERISTICS:
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Keller, Reinhold
TIILE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bended eysting bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sato, Selji
APPLICANT: Higashikuni, Naohiko
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kondo, Masaaki
APPLICANT: TITLE OF INVENTION: DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THITE FILLS THE FILLS THE STATE THE 
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Firmegan, Henderson, Farrabow, Garrett, 8
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      Losgich 1175
Cuery Match
Best Local Similarity 100.0%; Pred. No. 1.4c-44;
Matches 86; Conservative 0; Mismatches 0;
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CORRENT APPLICATION NUMBER: US/09/285,630A
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: JP16-87339/1996
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
LENGIH: 130
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| 1111-1,1111-1,111-1,111-1
| 1111-1,1111-1,111-1,111-1
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Patent No. US20013021515A1
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Patent No. US20020156234A1
GENERAL INFORMATION:
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STATE: D.C.
COUNTRY: USA
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US-09-947-563-5
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LOCATION: (92)
OTHER INFORMATION: Xaa equals any of the naturally occurring Leading dolds
NAME/KEY: SITE
LOCATION: (105)
OTHER INFORMATION: Xaa equals any of the naturally occurring Leading dolds
NAME/KEY: SITE
LOCATION: (124)
OTHER INFORMATION: Xaa equals any of the naturally occurring Leading which
NAME/KEY: SITE
LOCATION: (132)
OTHER INFORMATION: Xaa equals any of the naturally occurring Leading solds
NAME/KEY: SITE
LOCATION: (144)
OTHER INFORMATION: Xaa equals any of the naturally occurring leading dolds
NAME/KEY: SITE
LOCATION: (145)
OTHER INFORMATION: Xaa equals any of the naturally occurring leading dolds
NAME/KEY: SITE
LOCATION: (145)
OTHER INFORMATION: Xaa equals any of the naturally occurring leading dolds
LOCATION: (165)
OTHER INFORMATION: Xaa equals any of the naturally occurring leading dolds
US-09-925-297-865
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Search completed: September 15, 2003, 12:23:35 Job time : 36.0645 secs

Query Match Best Local Similarity 96.7%: Pred. No. 9.74-77: Matches 58; Conservative 6; Mismatches 2; Indels

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583.264 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sectore version 5.1.6
Copyright (c) 1993 * 2003 Compagen 1781
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A; Residues: 57-87 < CVED.

R; Ko, A.; Smyth, D.G.: Markussen, J.; Sundby, F.

Bur, J. Biochem, 20, 190-199, 1972

A; Title: Amino acid sequence of the C-peptide of numss profisuils.

A; Reference number: A91186; MUL:71257722; PMID:5560404

A; Accession: A91186

A; Molecule type: proteis.

A; Residues: 57-87 < KKOA>

R; Lucassen, A.M.; Julier: C.; Boressi, J.P.; Roftard, C.; Froquel, F.; Lathrop, M.; Bell, Nature Genet, 4, 355-310, 1993

A; Title: Susceptibility to insulm dependent dishesus mellitus maps to a 1.1 kb seament A; Molecule susceptibility to insulm dependent dishesus multiples and translated from GB/EMBL/JuH;

A; Reference number: 158114; MJL:9346428; PMID:835646

A; Reference number: 158114

A; Status: preliminary: translated from GB/EMBL/JuH;

A; Status: preliminary: translated from GB/EMBL/JuH;

A; Molecule type: DNA

A; Residues: 1-59-83-110 < RESS

A; Cross-references: GB:Li5440; NID:9307671; PTDN:AAA59179.1; PTDU:930772

R; Sieber; F.; Kamber, B.; Bartmain, A.; Jochl, A.; Siliker, B.; Rithel, W.

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A)Contents: annotation: synthesis of residues 57-87
R)Kaufmann, J.E.; Tranger, J.C.; Halban, P.A.
B)Contents: J. 310, 869-874, 1995
A)Tile: Sequence requirements for proinsulin processing at the B-chain/2 pyptide junctify A)Reference number: $58661; MUID:96013185; PMID:7555420
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Alfitle: The synthesis of C-peptide of facts profission.
A) Reference cumber: A91658; MJ10:75945057; PMID-469 3504
A) Contents: annotation: synthesis of residues $7.87
A) Contents: R.J. adeger, G.J. Kochia, W.
Chem. Bor. 106, 2347-2352, 1247
A) Title: Synthesis of the complete sequence of human proinsulin Ceperide.
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Best Local Similarity 106.0
Matches 86: Conservative
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Cispectes: Dercoptiecus actitions (green monkey, grivet)
Cispectes: Dercoptiecus (green monkey, grivet)
Cispectes: Dercoptiecus (green monkey)
Cispectes: Dercoptiecus (grivet)
Cispectes: Dercoptiecus (
Mol. Biol. Evol. 9, 193-203, 1992
A/Tille: Sequences of primate insulin genes support the hypothesis of a slower rate A/Reference number: A42179; MUID:92219953; PMID:1560757
A/Recession: A42179; MUID:92219953; PMID:1560757
A/Recession: 442179; MUID:92219953; PMID:1560757
A/Recession: 442179; MUID:921953; PMID:1560757
A/Recession: 1-110 cSEL>
A/Recession: A/Recess: EMBL:X61089; NID:938251; PIDN:CAA43403.1; PID:938252
A/Recession: 63/2
A/Recession: 63/2
C/Genetics: 63/2
C/Superfemily: insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 FVNQHLCGSHIVEALYLVCGFRGFFYTPKTRREAEDLQVGQVELGGSPGAGSLQPLALEG
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Pred, No. 1.6e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 463; DB 2;
100.0%; Pred. No. 2.8e-43;
iive 0; Mismatches 0;
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A:Molecule type: protein
A:Molecule type: Drotein
A:Residues: 25-54;00110 <SMIT>
A:Residues: 25-54;00110 <SMIT>
J: Biol. Chem. 247, 4866-4871, 1972
A:Title: Determination of the amino acid sequence of the monkey, sheep, and dog pr
A:Reforence number: A92111; MUID:72258016; PMID:4626369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: protein
A; Resioucs: 1-30;66-86 < HAR>
R; Tager, H.S.: Steiner, D.F.
B. J. Biol. Chem. 247, 7940, 1972
A; Tille: Primary structures of the proinsulin connecting peptides of the rat and h
A; Reference number: A92120; MUID:73061498; PMID:4640931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:IIIe: Cloning and nuclectide sequence analysis of the dog insulingene. Coded A:Reference number: A92413; MUID:83109071; PMID:6296142
A:Accession: A92413
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C.Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C.Dates: 13-Jul-1980, A92120
Arcession: A01580, A92120
A:Harris, J.I., Sanger, F., Naughton, M.A.
Arch. Blochem. Blophys, 65, 427-428, 1956
A;Title: Species differences in insulin.
                                                                                                                                                                                                                                                                                                                                                                                               1-11111 | 111-1113 | 11111 | 111 | 111 | 111 | 111 | 11 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
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A:Reference number: A90029; MUID:66160119; PMID:5949593
A:Accession: A01587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 110;
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A:Residues: 65-85 'I',87 <PET>
C:Superfamily: insulin
C:Keywords: hormone; pancreas
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-54/Typmain: insulin chain B #status experimental <
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89.5%; Pred. No. 2.9c-38;
tive 1; Mismatches 8
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                                                                      85 ALCKRGIVECCUS (CSLYCLENYCN 110
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Rest Local Similarity 89.5%
Witches 77: Conservative
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A; Accession: A01580
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A;Residues: 1-110 <SMI>
                                                                                                                                                                                                                                                                                                                                                                 cosmile precursor - dog
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                                                                                                    :::
Insulin precursor - crab-earing macaque
C:Species: Macaca fascionaris (crab-earing macaque)
C:Species: Macaca fascionaris (crab-earing macaque)
C:Species: 07-58p-1990 | Regimence_revision 37-58p-1990 | Ftext_change | M. 201-1960 |
C:Accession: J00178 | Reference | M. 1962 |
R:Wetekam | W.: Gronoberg | J.: Leineweber; | M.: Wenteumayer; | F.: Winnacker; | E... |
Gene 19, 179-183; | 1962 |
A:Title: The inclocitide sequence of chan coding for preprofishils from the primate Macacasion: J00178 |
M:Reference number: J00178 | MUTD:83080474; | PMID:8184882 |
A:Recession: J00178 |
A:Relatues: 1-110 | WHEP |
A:Relatues: 1-110 | WHEP |
A:Relatues: 1-110 | WHEP |
A:Cross-references: GB:J00386; | N:D:9342121: FIEN:AAA6649:: PID:4342122 |
C:Superiomity: Insulin | B:Status predicted | ASTD |
F:J25-44/Domain: Signal | B:Status predicted | ASTD |
F:J55-84/Domain: insulin chain | #status predicted | ACCH |
F:31-96,43-109,95-100/Disuifide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ú
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NiAlternate names: proproiosulin

NiAlternate names: proproiosulin

CiSpecies: Oryctolaques cuniculus (domestic rabbit)

CiDate: 24-Apr-1984 #sequence_revision 25-Aug 1997 #text_chauge 18-Jun-1939

CiAccession: A53438; A01581

CiDate: 24-Apr-1984 #sequence_revision 25-Aug 1997 #text_chauge 18-Jun-1939

CiAccession: A53438; A01581

Airtite: Insulin quoe expression and insulin synthesis in mammalian neuronal relis.

Airtite: Insulin quoe expression and insulin synthesis in mammalian neuronal relis.

Airtite: Insulin quoe expression and insulin synthesis in mammalian neuronal relis.

Airtite: Airtite:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVCQVHLGGGPGAGSLQPLALEG 50
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A)Accession: A01881
A)Molecule type: protein
A)Residues: 25-54;90-110 (SMI)
C)Superfamily: insulin
C)Superfamily: insulin
C)Superfamily: insulin
C)Superfamily: insulin chain B *totus predicted (SIG)
F)25-54;90-110/Product: insulin *status experimental (APC)
F)25-54;90-110/Product: insulin *status experimental (APC)
F)390-110/Domain: insulin chain A *status experimental (APC)
F)31-96,43-109,95-100/Disulfide bonds: *status predicted
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Pred. No. 1.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.5%: Score 456;
98.8%: Pred. No. 1
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Best Local Similarity 90.7*
These 78; Conservative
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A:Titie: Reversed-phase high-performance liquid chromatographic analyses of insulin
A:Reference number: A6:012: WJID:89292078: PMID:2661585
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Cyspecies: Was masculus (house mouse)
Cyspecies: Was masculus (house mouse)
Cyspecies: War 1952 #sequence_revision 14.Jul-1994 #text_change 18-Jun-1999
Cyspecies: Anar.1992 #sequence_revision 14.Jul-1994 #text_change 18-Jun-1999
Cyspecies: As6172: A661012: B01592
P.Weitworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.
T.Weil Evol. 23, 305-312, 1986
A.T.Llo: Characterization of the two nonallelic genes encoding mouse preproinsulin.
A:Reference number: A92965; MUID:87169768; PMID:3104603
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P:Suwa, T.: Obqaku, S.: Morioka, H.; Yanc, S.
Nol. Endocrinol. S. 61-67, 1990
A:Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the A:Reference number: A48172; MUID:90372989; PMID:2977023
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A:Residues: 57-87 <LIN>
A:Buenzli, H.F.; Glatthaar, B.; Kinz, P.; Muelhaupt, E.; Humbel, R.E.
Hoppe-Seyler's Z. Physiol. Chem. 353, 451-458, 1972
A:Ttle: Amino acid sequence of the two insulins from mouse (Mus musculus).
A:Reterence number: A01592: MUID:72189455; PMID:5063718
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                                                                                                                                                                                                                                                                                                                            Length 110;
                                             Score 394; DB 1; Length 110;
Pred. No. 9.2e-36;
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84.9%; Pred. No. 9.2e-36;
tive 4; Mismatches 9; Indels
                                                                                                                                                              9: Indels
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A.Residues: 25-54;90-11C <BUE>
Genetics: 34:90-11C <BUE>
C.Grotics: 63/1
C.Superfamily: insulin
C.Keywords: hormone; pancreas
F:1-24/Domain: signal sequence #status predicted <SIG>F:25-54/Domain: insulin chain B #status experimental <BCH>F:25-54/Domain: insulin #status experimental <BCH>F:25-54/Domain: insulin chain B #status experimental <BCH>F:25-54/Domain: insulin #status experimental <BCH</BCH
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E:Linde, S.: Nielseu, J.B.; Hansen, B.; Welinder, B.S.
J. Chromatogr, 462, 243-254, 1989
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                                                                                                                                                              4; Mismatches
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                                             85.1%;
64.9%;
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Best Local Similarity 84.9%;
Matches 73; Conservative
                                             0uery Match
Best Local Similarity 64.99
Matches 73; Conservative
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A;Residues: 1-110 <WEN>
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                                             A:Molecule type: protein

*Residues: 33-53 < TAGS

C:Gomment: Ys at positions 31-33 and 64-65 represent paired basic residues assured (by C:Superfamily: insulin

C:Superfamily: insulin

C:Superfamily: insulin

C:Superfamily: insulin

F:1-30/Pomain: insulin chain B *status experimental <MAT>

F:1-30/Pomain: insulin *status experimental <MAT>

F:33-65/Pomain: connecting peptide *status experimental <AGEP>

F:66-86/Domain: insulin chain A *status experimental <AGEP>

F:66-86/Domain: insulin chain A *status experimental <AGEP>

F:77-72,19-85,71-76/Disulfide bonds: *status predicted
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Almolecule type: DNA
Almolecule type: DNA
Alcross references: GS-200748; NID:g204958; PfDN:AAA41443.1; PTD:azci4455
Alcross references: GS-200748; NID:g204958; PfDN:AAA41443.1; PTD:azci4455
R:Steiner, D.F.; Clark, J.L.; No.an, C.; Rubenstein, A.H.; Marqollash, E.; Aren, H.;
Recent Prog. Horm, Res. 25, 207-282, 1959
Ajiitle: Proinsulin and the biosynthesis of insulin.
A;Reference number: A94231; MUID:70067613; PMID:4311936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin 2 precursor - rat
Cispecies: Rattus norvegious (Norway rah)
Cispecies: Rattus norvegious (Norway rah)
Cispecies: Rattus norvegious (Norway rah)
Cispecies: Rattus norvegious (1900 Missen rah)
Cispecies: Rattus norvegious (1900 Missen rah)
Cispecies: Rattus 1900 Missenthal, No. Efstratiadis. An Giltert, No. Kolodier, Bor Tinaro-Cell 18, 545-558, 1907
Affile: The structure and evolution of the two complete rat preprendents annex.
A:Reference number: A90789, Millow80045035; PMID498284
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A.Residues: 25-54:90-110 <STE>
R.Fager, H.S.; Steiner, D.F.
B.F. Steiner, D.F.
J. Biol. Chem. 247, 7936-7940, 1972
A.Title: Primary structures of the proinsulin connecting peptides of the rat. A.Reference number: A92120, MJLD:73061498; PMID:4647931
A.Rocession: C92120
A.Molecule type: protein
A.Residues: 57-87 <TAG>
R.Lomedico, P.T.; Rossenthal, N.; Kolodner, R.; Efstratladis, A.; Gilbert, W. R.Lomedico, P.T.; Rossenthal, A. 425-432, 1980
A.Title: The structure of rat preproinsulin genes.
A.Reference number: 151945; MJD:80240379; PMID:6245167
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A Residues: 1-110 <RES>
A Cross-references: GB:M25595, NID:9204550; PIDN:AAA41446.1; PID:9204952
GGenetics:
A:Genetics:
A:Genetic
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Pred. No. 7.26-36;
1; Mismatches 12; indels
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A,Status: preliminary; translated from GB/EMBL/DDRJ
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Best Local Similarity 84.9%
Therhos 73; Conservative
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A:Accession: A92120
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As Residues: 1-116 <CCR>
Astronomical Relations of the Stratiatis, Astronomical Relations of the Research Resident Residence For Bookenhal, R.; Efstratiatis, A.; Gilbert, W.; Kolodner, R.; Tizard Coll 18, 545-558, 1379
Astronomical Residuation and evolution of the two nonaliditerat preproinsuling eness Association compacts Association and PRESE RATES RATES ASSOCIATION AND ASSOCIATION ASS
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A Monocute type: protein
A:Residues: 25-54:90-110 (STE>
B:Tager: H.S.: Steiner, D.F.
J. Biol. Chem. 247, 7336-7440, 1972
A:Tile: Primary structures of the proinsulin connecting poptides of the rat and h
A:Reference number: A92120; MOID:73061498; PMID:4640931
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Cispecies: Sis scrota domestica (domestic pig)
Cispecies: Sis scrota domestica (domestic pig)
Ciscession: No.1581: Aspecies-revision 22-Jun-1981 #text_change 16-Jul-1999
Richanne, R.E.: Ellis, R.M.: Bromer, M.W.
Science 161, 165-167, 1968
A.Title: Percipe proinsuin: characterization and amino acid sequence.
A.Reference number: A94240: MCIP:68286488; PMLD:5657063
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A,Residues: 57-87 <TAG>
R;iomedico, P.T.: Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Gilbert,
Ann. N. Y. Acad. Sci. 343, 425-432, 1980
A:Title: The structure of rat preproinsulin genes.
A:Reference number: 151945; MUID:80240379; PMID:6249167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Molecule type: DNA
A:Res:30.2016 (2004)
A:Res:30.2016 (2004)
A:Cross-references: GBA:200747; NID:g204956; PIDN:AAA41442.1; PID:g204957
A:Cross-references: GBA:200747; NID:g204956; PIDN:AAA41442.1; PID:g204957
A:Steiner, D.F.; Glark, J.L.; Nola:, C.; Rubenstein, A.H.; Margoliash, B. Recent Prog. Horm. Res. 25, 207-282, 1969
A:Elle: Proinsulin and the Jossynthesis of insulin.
A:Reference number: A94231; MG1D:70067613; PMID:4311936
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Best Local Similarity 83.7%; Pred. No. 8.8e-35;
Matches 72; Conservative 4; Mismatches 10;
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A;Residues: 1-34,'0',36-84 <CHA>
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A;Residues: 1-110 <RES>
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                                                                                                                       Insulin precursor - deuroncouli
Cispecies: Advis Irlvingatis (dominionia, Liqin monkay, awl markay)
Cispecies: Advis Irlvingatis (dominionia, Liqin monkay, awl markay)
Cispecies: 27-Nov-1891 #sequence_revision 27 Nov-1891 flow, careession: A3988
Riseino, S.; Steiner, D.F.; Bell, G.T.
Proc. Natl. Acad. Sci. 18.5.A. #44. 7423-7427, 1947
A-Title: Sequence of a New Morld primate Hisulin Baylor low biological potency and image
A; Reference number: A39863; MUD:8804119; PMID:318367
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C)Species: Rattus norvegicus (Norway rat)
C)Species: Rattus norvegicus (Norway rat)
C)Bate: 23-0ct-1981 #sequence_nevision 23-0ct-1981 #text_change 24 Shp-1993
C)Accession: A90786, A90789; A94231; B92120; 151945; A01589
RCOrdell, B.; Bell, G.; Tischer, E.; DeNoto, F.M.; Ullrich, A.; Bistot, P.; Rutter, Octl 18, 533-543, 1879
A)Title: Isolation and characterization of a choned rat (nsulin gene.
A)Reference number: A90788; MCID:80045034; PMID:498283
A)Accession: A90788
A:Molecule type: DNA
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02-Jul 1996 #text_change 16 Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 FVNQHIJGGSBLVBALYIVGGBRAPPYTPKSRKGVBGQVAVGIBGGBRAPAGIGGTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Status: preliminary
A)Molecule type: DNA
A)Molecule type: DNA
A)Residucs: 1.108 <3EI>
A)Cross-references: GB:J02989; NID:q176555; PIDN:AAA\S74.1: PID:g176555
C)Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :4
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84.9%: Pred. No. 1.5e-35:
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84.5%; Pred. No. 1.56-35;
Wormartins 7;
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ses 73; Conservative
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Matches 73: Conserv
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Matches
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A:Molecule type: protein
A:Residues: 57-82 - 65AL>
A:Sanger, F:: Thompson, E.C.P.
Biochem, J. 53, 366-374, 1953
A:Titie: The amino-acid sequence in the qlycyl chaim of insulin. 2. The investigati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Reference number: A90342
A:Accession: A90342
A:Mo.coule type: protein
A:Residues: 85-105 <SAN>
R:Sauger, F: Tuppy, H:
H:Occem. J: 49, 481-490, 1951
A:Title: The amino-acid sequence in the picenylalanyl chain of insulin. 2. The inves
                                                                                                                                                                                                                              A.Title: Bovine proinsulfi: amino acid sequence of the C-peptide isolated from panca, Reference number: A91185; MOID:71257721; PMID:5105368
A,Accession: A91185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARILLE: Site-specific oxidation of histidine residues in glycated insulin mediated AREGENERC number: S48184; MUID:9433378; PMID:8055951
ARACCESSION: S48184
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                                                           A:Wolecule type: protein
A:Residues: 57-82 cSTE:
K:Salodangas, A.: Smyth, D.G.; Markussen, J.; Sundby, F.
Eur. J. B.cochem. 20, 183-189, 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.2%; Score 366.5; DB 1
80.2%; Pred. No. 8.7e-33;
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P.Cheng, R.: Kawakishi, S.
Evr. J. Blochem. 223, 759-764, 1994
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A:Molecule type: protein
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Best Local Similarity
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A; Status: preliminary
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C.Species: Bos primiganius taurus (cattie)
C.Saccession: A40909, A92080, A92074; A91185; A90342; A90341; S48184; S48185; S46288; A01
R.P. Agostino, J.; Younes, M.A.: White, J.K.; Besch, P.K.; Field, J.E.; Frazier, K.L.
Mol. Endocrinol. 1, 327-331, 1987
A.Title: Cloning and nucleotide sequence analysis of complementary decxyribonocicle acid
A.Reference number: A40909, MJD:88288209; PMID:2456452
A.Accession: A40909
A.Moclecule type: mRNA
A.Residues: 1-105 ADA>
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A;Mesidudes: 33-38,40-62 <SNE>
A;Note: the authors report the characterization of a connecting peptide variant lacking
A;Accession: B60835
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A.Residues: 25-105 <NCL>
A.Residues: 25-105 <NCL>
B.Steiner, D.F. Oyor, P.E., Terris, S.: Peterson, d.D.: Ribenstein, A.H.
J. Biol. Chem. 245, 1365-1374, 1971
A.Title: Isolation and characterization of proinsulin C-peptide from havine pancreas.
A.Reference number: A92074; MUID:71116469; PMID:5545089
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86.6%; Pred. No. 1.1e-34;
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                                                                                                                                                                                                                                                                                                                                                                                             A)Residues: 1-30:31-51 <BRO>
R)Snel, L.; Damgaard, U.
Horm. Metab. Res. 20, 476-480, 1988
A)Title: Proinsulin heterogeneity in pigs.
A)Reference number: A60835; MJIC:89032178; PMJD:3181865
A, Accession: A94572
A: Molecule type: protein
A; Residues: 1-84 -CH22-A
A; Residues: 1-84 -CH22-A
B; Bothem: J. 60, 556-565, 1955
B; Brown: H: Senger, F: Kitai, R.
Biochem: J. 60, 556-565, 1955
A; Ittle: The structure of pig and sheep insulins.
A; Accession: S16492
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Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-30;31-51 <BRO>
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Cypecies: Mas Buschlus (house house)

Cypecies: Mas Buschlus (house house)

Cycession: 826342 A66122 A06122 BELLIZ

Cycession: 826342 A66122 A06122 BELLIZ

Symbologics: 84412 A66122 A06122 BELLIZ

J. Mol. Evol. 21, 304-124 106

A. Millich Evol. 21, 304-124 106

A. Mccession: 56434 A6612 A06122 BELLIZ

A. Molecule type: INA

A. Mccession: 56444 A. Millich Evol. 61, 104 Evol. 61, 104 Evol. 104 Evol. 61, 104
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TISSUE=Pancreas;
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RESULT I
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between the swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                            25 FVNQELGGSHLVERALYLVGGERGFFYTPKTRRPAEDLOVGQVELGGGPGAGSLQPLALEG 84
    1 FVNOHLOSSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGFGAGSLQPLALEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.; "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 247:4866-4871(1972).

-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CEGI, PERMEABILITY TO MONOSACCHARIDES. AMINO ACIDS AN FATTY ACIDS. IT ACCELERAIES GLYCOLYSIS, THE PENTUSE PHOSPHATE CYCLE. AND GLYCOGEN SYNTHES:S IN LIVER.

-!- SUBGNII: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISCLETURE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa: Chordata: Craniata: Vertebrata, Eutoleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Cercopithecidae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92219953; PubMcd-1560757;
Seinc S., Bell G.I., Li W.;
"Sequences of primate insulin genes support the hypothesis of
"Sequences of primate insulin genes support are of molecular evolution in humans and apes than in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
                                                                                                                                                                                                                                                      INS_CERAE STANDARD. FRT; 110 AA. PP.0407: PU.1909; 01-APE-1593 (Rei. 25, Created) (M. APE-1993 (Rei. 25, Cast sequence update) 01-FEB-1996 (Rei. 33, Cast annotation update)
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                                                                                                                     SLOKEGIVECCTSICSLYQLENYCN 310
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PIR: 942179; B42179.
HSSP; P01308: 1A10.
Interpre: IPP054925; Ins/IGF/relax.
Pfam; PF05049; Insulin; 1.
SMART; SM09078; I1GF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE OF 57-87.
MEDLINE-72258016: PubMed-4626369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monkeys.";
Mol. Biol. Evol. 9:193-203(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae, Cercopithecus.
NCBI_TaxID-9534;
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1. SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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                                                                                           1 FVNQHLOGSHLVEALMI VQGRROFFYTPK PRRBABILLOVSUVBIASSHOARSIJJFLALBAR 🚓
                                                                                                                     Gaps
                                                    -IT FUNCTION: INSULIN DEGERAGES BLOOD GLUCOSE CONCENTRATION, IT INREASES CELL PERMEAFLLIY TO MONGSACCHARIDES, AMING ACLUS AND FATTY ACLUS. IT ACCELERATES GLYCOLKSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-IT SUBGNIT: HETEROSIMER CF A B CHAIN AND AN A CHAIN LINKED HY TWO
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Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostoni;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92219953; PubMed-1560757; Seino S., Bell G.I., Li W.; "Sequences of primate insulin genes support the hypothesis of slower rate of molecular evolution in humans and apps than in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 463; 35 1; Length 110; 100.0%; Pred. No. 9.2e-43;
    Leagth 11
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O
100.0%; Score 463; LP 1:
100.0%; Pred. No. 5.26.43;
Live 3; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
61-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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PDB: IBFE: 29-MAR-66.
INCEPTO: IPK004825; INS/IGF/relax.
PFEM: PFC0049; ISSCILD: 1.

PRINTS: PRO0277; INSULINS.
SMART: SM00078; IIGF: 1.
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                       Best Local Similarity 100.
Matches 86, Conservative
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Matches 86; Conserv
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P30410;
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Mol. Biol
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                                                                                                                                         1 FVNQHIGGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGRGAGSLQPLALEG (4)
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                                                                                                                                                                 25 FVNQHLGGSPHLVEALYLVGGERGFFYTPKTRRRAEDPQVGQVELGGGFGASG;QPLALEG
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CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;
Mammalia; Eutheria; Primates; Catarrbini: Ceropithecidae;
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                       Score 456; ER 1: Longth 110:
Pred. No. 5.2e-42;
0: Mismatches 1: indels
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Wetekam M., Groneberg J., Leinewebei M., Wendenmayer F.,
Winnacker E.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11991 MW; 83C6E33A80A420F9 CBC64;
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HSSP: P0178: IAIG.

InterPro: IPR004825: Ins/ICF/relax.

PRINTS: PR00277: INSULINE.

SMART: SM0078; IGF. 1.

PROSITE: PS00262: INSULINE.

ILSULIN family Hormone: Giucose metabolism: Signal.

SIGNAL
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No. 5.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F30406 Pt1309;
21-301-1986 (Rel. 01, Created)
13-AJG-1987 (Rel. 05, Last sequence update;
13-FEB-1996 (Rel. 33, Last ennotation update;
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Pred. No. 5
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Gene 19:179-183(1982).
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                                                       98.88
                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae: Macada.
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                          Ouery Match
Best Local Similarity
Matches 85: Conserv
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98.389 98.89

Query Match Best Local Similarity

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                                                                                     1 FUNDHEGGSHLVEALYLVCGERGFFYTPKTRREABDLUVGQVBIGSGPGAGSIQPLALEG 69 (1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Insulin gene expression and insulin synthesis in mammalian neuronal
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GLGGINGS S.J., Carnaghi L.R., Devaskar S.G.;
Substreed (APR-1991) to the EMBL/Genback/Obbi
-:- FJNCTION: INSULIN DECREASES BLOOD GLGGOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AKINO ACIDS AND
FATTY ACIDS. 1T ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-:- SUBJUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULEIDE BONCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crycholaqus cuniculus (Rabbit).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-New Zealand white; IISSUB-Pancreas;
MEDLINE-94.79230; PubMed-8128571;
Medeskar S.U., Glddings S.J., Rajakumar P.A., Carnaghi L.R.,
Menos R.K., Zahm D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Species variation in the amino acid sequence of insulin."; Am. J. Med. 40:652-668(1966).
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-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
1; Indels
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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C PEPTIDE.
INSULIN A CHAIN.
0; Mismatches
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MEDIINE-66160119; PubMed-5949593;
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SMART: SM00078: I1GF: 1.
PROSITE: PS00262; INSULIN;
85; Conservative
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87
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HSSP; P01308; 1TYN
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                                                                                                                                                                                                                      1 FVNORLGGSHLVBALXLVGGBRGFFYTFKTRRARDLGVGGVBLGGBPAGSTLQFDLAFFFF 11 HTT 11 HTT 11 TT 125 FVNORLGGSHLVBALXLVGGBRGFFYTFKSRRRVFFLQVGGRRUGGSPGAFT GFSST. B1
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Am. J. Med. 40:652-666(1965).
-!- FUNCTION: INSCLIN DECREASES BLOOD SINGOSE CONCENTRATION. IT
INCREASES CELL PERMEAHILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT ACCELEMATES GLYCOLESS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis,
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KWOK S.C.M., Chan S.J., Steiner D.F.;
"Cloning and nucleotide sequence analysis of the dog insulin g
Coded amino acid sequence of canine preproinsulin predicts an
                                                                                                                                        Length 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULPIDE BONDS.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMELARITY: BELONGS TO THE INSULIN/IGF/RECANIN FAMILY.
                                                                                                                                                                               5; Indels
                                                                  E -> Y (IN REF. 3).
82D2975885D77PA8 CR064;
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SIGNAL 1 24
                                                                                                                                   91.6%; Score 424: DB 1; 90.7%; Pred. No. 1.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last Sequence update)
01-FEB-1996 (Rel. 33, Last amnotation update)
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                                                                                                                                                                               3: Mismatches
  INTERCHAIN
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                         INTERCHAIN
                                                                                                                                                                                                                                                                                                             61 SLOKRGIVEGOGISTOSLYGLENYCN 86
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Pram, Pr0049; Insulin; 1.
SMART; SW0078; ILGF: 1.
PROSITE: PS00262; INSULIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al C-peptide fragment.";
Chem. 258:2357-2:63(1983).
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MEDLINE-66160119; PubMed=5949593;
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                                                                                                              Ouery Match
Best Local Similarity 90...
Thes 78: Conservative
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96
169
160
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31
43
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110 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nsulin precursor.
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                                         DISULFID
CONFLICT
SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                            1 FVNOHLGGSHLVFALYLVGGEKGFFYTPKTRREAEDLQVGQVELGGGGGGGGGLQPLALEG 60
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tredrea M.M., Buck M.J., Guhaniyogi J., Squire I.L., Andrews M.T.;
"Regulation of PDK4 expression in a hibernailing mammal.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS.
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-!-SUBUNIT: HETBEROPIKER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spormophilus tridecemlineatus (Thirteen-lined ground squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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G
                                                                                                                                          Length 110;
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-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                     12190 MW; A574791864A4FB98 CKC64;
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                                                                                                                                          Score 417; DB 1;
Pred. No. 7.7e-38;
1: Mismatches 8
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INSULIN B CHAIN.
C PEPTIDE.
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[5-SEP-2003 (Rel. 42, Last sequence update)
[5-SEP-2003 (Rel. 42, Last annotation update)
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                   INSULIN A CHAIN.
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                                         INTERCHAIN.
                                                              INTERCHAIN.
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PROSITE; PS00262; INSCLIN; 1.
                                                                                                                                              900.000
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                                                                                                                                                               Local Similaries
es 77; Conservative
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                                                                                                     110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-43179;
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-!- SUBUNIT:
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                                                                             25 FVNQHLGSSHLVBALYLVGGERGFFYTPKSRREVENDGGQVELGGGFGAGLFQFLAGER #4
                                                            1 FVNQHLCGSHLVEALYLYCGERGFFYTPKTRREAEDLQVGQVELGGGFGAGSLQFLALEG 60
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"Primary structures of the proinsulin connecting populdes of the latter the forse.";
and the forse.";
J. Biol. Chem. 247:7936-7940(1972).
-1- FUNCTION: INSULIN DECREASES BLOOD GLUCGE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MOUSACCHARIES. AMIND ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCOLNSIS, THE PENTOSE PHOSPHAIR
CYCLE. AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/GEFRENAXIN FAMILY.
-:- CAUTION: X'S AT POSITIONS 31-32 AND 64-65 REPRESENT FATERL HASTO RESIDEDS ASSUMED BY HOMOLOGY TO BE PRESENT IN THE PRECURSOR MOLECULE.
                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa: Chordata, Craniata: Vercebrata: Butoloostomi.
Mammalia, Eutheria: Perissodactyla: Equidae: Eques.
                                 Ö
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SUBUKIT: HETEROLIMER OF A 3 CHAIN AND AN A CHAIN LINKED BY DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ
Score 413; EB 1; Length 110;
Pred. No. 2e-37;
3: Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 394; DB 1: Longth 86; Pred. No. 1.7e-45;
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                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 31, Created)
21-JUL-1986 (Rel. 31, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN B CHAIN.
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INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulia family, Hormone, Glucose metabolism.
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                                                                                                                                                                                                                                 32
                                                                                                                                     INTERCHAIN
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                                                                                                                       61 SLQKRGIVEQCCTSICS_YQLENYCN 86
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HISSP: PO1317; 1APH:
Interpro: 1PMO04825; Ins/IGF/relax.
Pfam: PF00049; Insulin:
SMART; SM00078: IIGF: 1.
                                                                                                                                                                                                                                 PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 33-63.
MEDIINE-73061498: PubMed:4640931;
89.2%
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-30 AND 66-85
               1 Similarity 89.5
77; Conservative
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                                                                                                                                                                                                                                                                                                                                     Equus caballus (Horse).
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Best Local Simi
Matches 73; (
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Employed Buoinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announcc.or scnd an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insulin family; Hormone; Glucose metabolism; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                            Nawa T., Ohgaku S., Morioka H., Yano S., Walecular cloning and DNA sequence analysis of preproinsulin genes in the NON mouse, an animal model of human non-obese, non-insulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBGULT: HETEROPIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULEIDE BONDS.
                                                                                                                                                                                                    Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                       MEDLINE-87169768, PubMed-3104663;
Wentworth B.M., Schaefer I.M., Villa-Komaroff I., Chirgwin J.M.,
"Characterization of the two nonallelic genes encoding mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/ISF/RELAXIN FAMILY.
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INSULIN 2 C PEPTIDE.
INSULIN 2 A CHAIN.
INTERCHAIN.
                                                                                                                   21-30L-1966 (Rel. 03, Created)
13-AUG-1967 (Rel. 05, Last sequence update)
15-OCT-2001 (Rel. 46, Last annotation update)
61 SLOKRGIVEGGGTSICSLYQLENYCN 86
              61 PQQXXGTVEOCCIGICSIAQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                    dependent diabetes mellitus.";
3. Nol. Endocrinol. 5:61-67(1999).
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90372989; PubMed+2397023;
                                                                                                                                                                                                                                                                                                               preproinsulin.";
J. Mol. Evol. 23:305-312(1986).
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SMART; SM00078; ILGF; 1.
                                                                                              STANDARD;
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INS2 OR INS-2.
                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Mammalia, Eutheria, Rodentia, Sciarognathi, Muridae, Muribac, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Spraque-Dawley, TISSUE-Liver;
MEDLINE-80045035: PubMed-496284;
Lomedico P., Rosonthal N., Efstratladis A., Gilbert W., Rolodner R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The structure and evolution of the two nonallelic rat preproinsulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-54 AND 90-110.
MEDLINE-70657613: Purbled 4311938;
Steiner D.E., Clark J.L., Nolan C., Rubenstein A.H., Margeliash E.,
Steiner D.E., Oyer P.E.;
*Proinsulin and the biosynthesis of insulin.";
Recent Prog. Horm. Res. 25:267-282(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-86310882: PURMed-2427930;
Soares M.B., Schin E., Henderson A., Karathannsis S.K., Cate R.,
Zeitlin S., Chiriwin J., Efstratiodis A.,
"RNA-mediated gene duplication: the rat proproinsalin I gene is
functional retroposon."
                                                                                                                           13
                                                                              Score 364: DR 1: Despth 110:
Pred. No. 2.2e-35;
4: Mismatches 3: Indels
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Comedico P.T., Rosenthal N., Rosenthal N., Rosenthal N.,
Gilbert N.,
"The structure of rat preprofusulis memos.".
                                              12364 MW: 355408803D24FDAD CBMC4
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Markusson J., Sundby F.:
"Rat-proinsulin C'Peptides. Amino-acid soquences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
      INTERCEPTA
                                                                                                                                                                                                                                                Ann. N.Y. Acad. Sci. 343:425:432(1980).
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                                                                                th RSimilarity 84.9%; 73; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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1007
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                                          1:0 AA;
                                                                                                        Sest Local Similarity
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INS2_RAT
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This SWISS-PROT energy is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way non-profit institutions as long as its content is in no way noticed and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or sond an email to license@lsb-sib.ch).
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Insulin family; Hormone; Glucose metabolism; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FVNQHT/GGS::LVEALY1/VCGEKGFFYTPKTRREAEDLQVGQVEL/GGGPGAGSLQPLALEG
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Sainris Sciureus (Common squirrel monkey).
Eukaryota: Metazoa: Chordata: Cremiata: Vertebrata: Euteleostomi:
Mammalia; Eutheria: Primates: Platyrrhini: Cebidae; Aotinae: Aotus.
--- FUNCTION: INSULIN DECREASES SLOCD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GIZCOLYSIS, THE PENTOSE PHOSPHATE CYCLE. AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88041119; PubMed-3118367;
Seinc S., Steiner D.F., Bell G.I.;
"Sequence of a New World primate insulin having low biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110;
                                                                                                                                                                                                 SUBCELEULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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84.9%; Pred. No. 2.2e-35;
ive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 INSULIN 2 B CHAIN.
87 INSULIN 2 C PEFIDE.
110 INSULIN 2 A CHAIN.
96 INTERCRAIN.
109 INTERCHAIN.
100
4, 12339 MW; 3A626DA98C86F3CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potency and immunoreactivity.";
Proc. Nati. Acad. Sci. U.S.A. 84:7423-7427(1987).
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01-JUL-1989 (Rel. 11, Last Sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR004825; Ins/IGF/relax.
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MBLL; M25583; AAA41440.1; JOINED.
PIR: 890769; IPRT2.
HSSP: PC1317; IAPH.
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SMART; SM00078; IIGF; 1.
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nes 73; Conservative
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G.I., Sanchez-Pescador R.;
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-:- SUBCELLULAR LOCATION: Socreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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                                                      SPECIES-S Sciurcis;

Mubbline-9/06899; Pubmed-22/4627;

Yu J. H., Eng J. Yalow B.S.;

Tisolation and amino acid sequences of squirrel munkey (Salmiti Sciurce) insulan and amino acid sequences of squirrel munkey (Salmiti Foulzed) insulan and alloaden.

From Mail Acad Sci. U.S. A. 87:4746-9768(1992).

FONCION: INSULIN DECREASES BLOOD GLUCOSE COMCENTANION. IT INCREASES CHIL PERMARMILITY MONOSACCHARIDES. AMINO ACIDS AND FATTY ACIDS. IN ACCELERATES GLYCOLYSIS, THE PENTOSE PROSPHATE CYCLE, AND GLYGORESIS IN LIVER.

FATTY ACIDS.

FORTILL HOSPINGER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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Mammalia; Eutheria; Rodentic; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
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INSULIN A CHAIN,
INTERCHAIN,
INTERCHAIN,
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InterPro; 1PR004825; Ins/IG:/relax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 84.9 les 73; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Rattus.
                                                                                                                                                                 -:- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CEL. PERREABILITY TO MONOSACCHARIDES, AKTNO ACIDS AND FATTY ACIDS. IT ACCELEARTES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNHESIS IN LIVER.
                                                                       SEGUENCE OF 25-54 AND 96-116.
Neclon F.A., Deforer H.K., Steinman H., Lebovitz H.E.;
Scructure of hamster insulin: comparison with a tumor insulin.";
Fed. Proc. 32:300-300(1973).
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Cordell B., Bell G.L. Thscher E. Denoto F.M., Ullrich A.,
Pictet R.L., Rutter W.J., Goodman H.M.;
"Isolation and characterization of a cloned rat insulin gene.";
"Sequence of a cDNA encoding Syrian hamster preproinsulin.";
Diabetes 33:297-300(1984)
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                                                                                                                                                                                                                                                                                                                   -:- SUBCELLUIAR LOCATION: Secreted.
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Pram: Pr00049; Insulis; 1.
SRART, SM00078: ILSt. 1.
SROSITE: PSC0262; INSULIN; 1.
Insulin family; Hormone: Glucose metabolism; Signal.
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16-OCT-2001 (Rel. 40, Last annotation update)
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C PEPTIDE.
INSULIN A CHAIN.
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HSSP: P01308; 1TYM.
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Matches 73, Conservative
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110
109
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INSI OR INS-1.
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Mamm. Genome 13:388-398(2002).
        83.28;
83.78;
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Coory Match
Bost Local Similarity 83.7%
Matches 72, Conservative
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Insulin family: Hormone: Glucose metabolism; Signal: Multigene tamily.
                                                                                                                                                                             fixand R.: The structure and evolution of the two conditable for preparations from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tager H.S., Steiner D.F., *Primary structures of the proinsulin connecting peptides of the run and the horse.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=72177385; PubMed=4554104;
MEDLINE=72177385; PubMed=4554104;
Markussen - 1., Sundby E.;
Markussen - 2., Sundby E.;
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Eur. - 5. Biochem. - 25:153-163(1972).
- 1- FUNCTION: INSULIN DECREASES BLOOD GLCCGSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACTIOS AND PATTY ACIDS. IT ACCERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYMIHESIS IN LIVER.
- 1- SUBGNIT: HETERODIMER OF A H CHAIN AND AN A CHAIN LINKED BY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-54 AND 90-110.
MEDLINE-70067613; PubMed-4111938;
Steiner D.F., Clark J.L., Nolum C., Rubenstein A.H., Margoliash E.,
Aten B., Oper P.E.,
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                                                                                                                                               Lomedico F., Rosenthal N., Efstratlados A., Tilbert W., Kolodner
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-80240379; PubMed-6249167;
Lomedico P.T., Roseuthal N., Kolodner R., Elstrafiadis A.,
Gilbert W.;
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULAN/IGE/RELAXIK FAMILY.
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INSULIN 1 C PEPTIBE.
INSULIN 1 A CHAIN.
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Pfam: PP00049; Insulin; i.
SMART; SM00078; IIGF; i.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-73061498; PubMed-4640931;
                                                                                          STRAIN-Spraque-Dawley: TISKUS-LL:
MEDLINE-60045035: FubMed-4%8284;
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EMBL: JC044; AA41442.::
EMBL: M25584; AA41439.!; .
PTR: A90788; IA7F.
HSSP: PC1308; 1A7F.
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     Cell 18:533-543(1979).
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                                                                     1 FVNQHLCGSHL/VEALYLVCGERGFFFTFKTRREAEDLQVGQVELGGGGPGASSLQPLALEG 60
                                                                                      MEDLINE=89099316; PubMed=2905485;
Baker E.N., Blundell T.L., Cutfield J.F., Cutfield S.M., Dodson E.J.,
Dodson G.G., Crowfoot Hodgkin D.M., Hubbard R.E., Isaacs N.W.,
Beynolds C.D., Sakabe K., Sakabe N., Vijayan N.M.;
The structure of Zan pig insulin crystals at 1.5.A resolution.";
Philos, Trans. R. Soc. Lond., B, Biol. Sci. 319:369-456(1988).
                                    Gaps
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INSACR N.W., Agarwal R.C.;
"Experience with fast Fourier least squares in the refinement of the
"Experience with fast Fourier least squares in the refinement of the
crystal structure of rhombohedral 2-zinc insulin at 1.5-A
                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota: Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
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Chance R.E., Ellis K.M., Bromer W.W.;
"Porcine proinsulin: characterization and amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative sequence analysis of the INS-IGF2-H19 gene cluster
                                    0:
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STRAIN-Large white:
MEDLINE-22135958; PubMed-12140686;
Amarger V., NGYPEN K., Laere A.S., Braunschweig M., Nezer C.,
Georges M., Andersson L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
Rlundell T.5., Dodson G.G., Hodgkin D., Mercola D.;
TISNILL. The structure in the crystal and its reflection in
chemistry and biology.";
Adv. Protein Chem. 26:279-402(1972).
 Length 110;
          2e-34;
-hes 10; ladels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Hen X.G. Tuch B.E.:
"Compiete protrine preproinsulin CDNA sequence.";
Submitted (MAY-1998) to the EMB:/Genbank/DDB3 databases.
Score 385; DB 1;
Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. Cl. Created)
16-OCT-2001 (Rel. 46, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
                                    4; Mismatches
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Chance R.E.;
Submitted (JUL-1970) to the PIR data bank.
                                                                                                                                                             : IIII :: IIII :: IIII IIIII | IIIII | 85 ARQKRGIVEQCCISTCSLYQLENYCN 110
                                                                                                                                         61 SLOKRGIVEQCCTSICSLYOLENYCN 86
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1 FVNGHLCGSHLVBALYLVCGERGFFYTPKTRREAEDLOVGOVELGGGPGAGSLOPLALEG
                                                          Score 383; DB 1; Length 108;
Pred. No. 3.3e-34;
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-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                             Indels
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INTERCHAIN (BY SIMILARITY).
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Pram; Pr0049; Insulin; I.
PRINTS; PR0627; INSULINB.
SMART; SM00078; ILGF; I.
PROSITE; PS00262; INSULIN; I.
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15-JUL-1998 (Rel. 36, Last anno
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                    Best Local Similarity 86.0 Matches 74; Conservative
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                                                                                                           Hormone, Glicose metabolism, Signal, 3D-structure,
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SIMILARITY BELONGS TO THE INSULNATISF/RELAXIN FAMILY.
BATARASE: NAME=PROTEIN SPOLITUINT:
NOTE=.Ssuc 9 of April 2001.
WWW="http://www.expasy.org/spotlight/aiticles/spulf.09.html"
         Balschmidt P., Hansen P.B., Dodson E., Dodson G., Korber P.;
"Structure of porcine insulin cocrystallized with chupeine R.":
Acta Crystalloar, B 47:975-986(1991).
                                                      MEDLINE-91222450; PebMed-2025410;
Badger J., Harris M.R., Reynolds C.D., Evans A.D., Dydson E.D.,
Dodson G.G., North A.C.T.;
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INTERCHAIN.
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C PEPTIDE.
                                                                                  "Structure of the pig insul.n dimer 1:. Acta Crystallogr. B 47:127-136(1991).
                                                                                                                                                                                                                                                                                                                                                      EMBL: AF064555; AAC77920.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro; IPRO54825; Ins/IGF/relax.
Pfam; PF50649; Insulin; 1.
SMARI: SMO607F- Time
MEDLINE=92126280; PubMed-1772633;
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16-JUN-97.
01-APR-98.
                                              X-RAY CRYSTALLOGRAPHY
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Button J.C., Gross D.C.;
Būkuryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
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Pred. No. 1.5e-33;
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70; Conservative	FWNOHLGGSHLVBALXLXTGERGFFYTPKTRREARCACOOOVETGGGGGGGGGGGGGGGGGGGAGGGAGGGAGGGAGGGAGG	25 PVNQHLGGSHLVEALTIYGGERGFFYTPKFRRGVGRGWFQLRLGGSRGGAGGGAATALEV + 0	SLOKRGIVECOCTSICSLYOLENYON 86	85 ARQKRGIVEQCCTGICSLYQLENYCN 110	Scarch completed: September 15, 2003, 12:01:30 Job time: 9.01434 secs
707	. i	25 FV	61 St.	85 AR	leted 9.014
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042289 oreochromiss
05327 peralichthy
093527 peralichthy
090360 cyprinus ca
08041 petromyzon
09356 melagaris g
099157 acanthopagr
09143 squalus aca
09126 oncorhynchu
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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Stead J.D.H., Jeffreys A.J.;
"Haplotype diversity at the insulin region.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AY:37503; AAN06937.1: -.
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Eukaryota, Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalla: Eutheria: Rodeniia; Sciurognathi; Sciuridae; Sciurinae;
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Felis.
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                                                                                                                                                                                                                                                                                                                                               Tredrea M.M., Buck M.J., Guhaniyogi J., Squire T.L., Andrews "Regulation of PDK4 expression in a hibernating memmal."; Submitted (JUN-2001) to the EMBL/GenBack/HDBJ databases. -- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). -- SIMILARITY: BELCNGS TO THE INSULIN/10F/RELAXIN FAMILY. HSSP; P01308; 11.NF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%; Score 41%; DB 11; Length 119; 89.5%; Pred. No. 3.4c-41; Live 3; Mismatches 6; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: SECRETEE (SV SIMITARITY).
-1- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
EMBL: AE043535: BAB84110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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"cat insulin.";
Submitted (MAY-2000) to the EMBL/GenBank/DDSL databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERMIS: PP00049: INSULIND: 1. PRINTS: PR0277: INSULIND. PRINTS: PR0277: INSULIND. SMART: SM00075: ILGF: 1. LGF: 1. PR051TE: PS00262: INSULIN: 1. SEQUENCE 110 AA: 12004 MW: 4511769D6622BEHS CHC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Cranista, Vertobrito,
Marmalia, Eutheria, Carnivora, Fissipedia, Felidac,
NCBI_TaxID=9685.
01-DEC-2001 (irEMBirel, 19, Last Sequence update)
01-MAR-2003 (TrEMBirel, 2), Last annotation update)
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Last Annotation update;
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83.7%; Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AA
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ds alokrgivedcotrice:xoldenych 1:0
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61-WAR-2002 (TEFWSLFC), 20, Last sequin 1-WAR-2003 (TEFWSLFC), 23, Last anno
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Best Local Similarity 83.75.
Three 72; Conservative
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Matches 77; Conservative
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Pancreas:
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                                                                                                                                                                                                 Spermophilus.
NCBI_TaxID-43179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        C'hUigin C., Tichy H., Klein J.; "Molecular evolution in higher primates; gene specific and organism specific characteristics."; "Submitted (MAR-2002) to UHE EMBL/GenBank/DDBJ databases. EMBL, AY092023; AAM76640.1: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Edigin C., Tichy H., Klein C., "Molecular evolution in higher primates; gene specific and organism specific characteristics."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY092024; AAM76641.1; ...
                                                                                                                                                                                                                                                                                                      Gorilla gorilla (gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eskaryola, Motazoa, Chordata, Cranjata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
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65 AA; 6920 MW: B772017FD8BCABEA CRC64;
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01-MAR-2003 (TrEMBLrel, 23, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.9%; Score 342; DB 6; 1
100.0%; Pred. No. 4.7e-33;
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PRT;
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                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                    3 NQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVCQVELGCGPCAGSLQPTALEGSL
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Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Pantodontidae; Pantodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiodon alosoidės (goldėye).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
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46.4%; Pred. No. 1.4e-19;
Live 14; Mismatches 13; Indels 25;
                                                                                                                                                                                             56.9%; Score 235.5; DB 13; Length 111; 54.1%; Pred. No. 3.7e-20;
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                                                                                                                                          SEQUENCE 111 AA; 12491 MW; AC9519D2D4865D20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61-JUN-2001 (IrEMBLrel. 17, Created)
61-JUN-2001 (TrEMBLrel. 17, Last sequence update)
61-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 AA
                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  S TATELLE SEE SEE STANDER STAN
                                                                                                                                                                                                                                                                                                                                                                                                                   63 O-KRGIVEOCCTSICSLYQLENYCN 86
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01-DEC-2001 (TFEMESTEL) 19, Last seq
01-MAR-2003 (TFEMESTEL) 23, Last and
Preproinsulin (Fragmont).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Pfam, PF00649; Insulin; I. PRINTS, PR06277; INSCLINB. SMART: SM00078; IIF: 1. PR0621E; PS00262; INSULIN; I.
                                                                                                                                                                                                                         54.18;
                                                                                                                                                                                                                                                     46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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01-JUN-2001
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0902Y1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1)
SEQUENCE FROM N.A.
MEDLINE-20362507; PubMed-10918274;
ILWID D.M., Sivarajah P.;
*Proinsulin cDNAs from the leopard frog, Rana pipiens: evolution of proinsulin processing.
                                                                                                                                                                                                                                                                                                                                             Rana pipiens (Northern leopard freq).
Eukaryota; Metazoa: Chordata; Graniata: Verrebrara: Burjelerstomn,
Amphibla: Batrachia: Anuri: Neobatrachia; Ranciden: Sanidar; Rann.
NCBI_TaxIb*8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordita, Craniata, Vertebrata, Euteleosturi):
Actinopterygii, Neopterygii, Toleostell estevilossemorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 53.2%; Score 246.5; UR L3; Length L65; Local Similarity 51.5%; Pred. No. 1.7e-21; nes 52; Conservative 9; Mismatches 7; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comp. Biochem. Physiol. 1258:405-410(2508).
-!- SUBCELGULAR LOCATION: SECRETED (BY SIMILARITY).
--- SIMILARITY: HELONGS TO THE INSULIN/TOF/REHAXIN FAMILY.
EMBL: AF227187. AAP87285.1; ---
ESSP: P01315; 18EB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AA; 12183 MW; 3A870EEC70217F92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGSELDEMOVOSOAFQKRKPGIVEOCCHNICSEYDLENYON 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-00T-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last. Sequence update)
01-NAR-2003 (TrEMBLrel. 24, Last annotation ipdate)
Preproinsulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (Tremstrel, 17, dast sequence update) 01-MAR-2002 (Tremstrel, 2), dast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osteoglossiformes: Osteoglossidae: Osteoglessim.
                                                                                                                                                                                                105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1 A.A.
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Ostooglossum bicirrhosum (silver alawana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-JUN-2001 (TrEMBLIEL, 17, Created)
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR0C4825; Ins/IGF/relax
Pram: PR00045; Insalin: 1
PRINTS: PR0C277: INSULINE
SMART: SM00078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004825; Ins/IGF/relax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21203577; PubMed=11305171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS03262: INSULIN: 1. SEQUENCE 135 AA: 12183 MW.
                                                                                                                                                                                             PRECIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                       IVEQC 65
17 DGAVI 73
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Q98TA7
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61 SL---
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                                                                                                                                                                OBDDES
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0902N4
                                                                                                                 RESULT 11
                                                                                                                                                                                    NATIONAL SERVICE SERVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 SQHLCGSHLVDALYMVCGEKGFFYQPKTKNVVD-------PLLGFLSFKSAJENS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NOHLGGSHLVEALYLVGSERGFFYTPK-TRREAEDLQVGQVELGGGPGAGSLQFLA-LEG (C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NOHICGSHLVEALYLVCGERGFFYTPKTRREAEDLOVGQVELGGGFGASSIQPIAL --- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.1%; Score 222.5; UB 13; Length 110;
45.4%; Pred. No. 1.3e/18;
tive 13; Mismatches 15; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21203577; FubMed-11306171;
A L-Kahrouki A.A. Irwin D.M. Grahn. L.C., Youson J.H.;
AL-Kahrouki A.A. Irwin D.M. Grahn. L.C., Youson J.H.;
Molechlar choing of preprintal nobles from several
costeoqlossomorphs and a ceptimid.
Mol. Cell. Endocrinol. 174:51-58(201).
C-1: SUBCELLGRAN LOCATION. SECRETED (NY GE/RELAXIN FAMILY).
C-1: SUBCELLGRAN LOCATION. SECRETED (NY GE/RELAXIN FAMILY).
R MSSP: POL308: LD.PH.
R RSSP: POL308: LD.PH.
R InterPro: IPRO04825; Ins/IDF/relax.
R PASRT: SM00078: 11GF: 1.
NON_IER.
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Actinopterygli, Neopterygli, Teleostel, Ostanglossomarpha:
Osteoglossiformes: Biodontidae: Hiodos.
                                                                                                     MEDLINE-21203577; PubMed=1130617;
Al-Mahrouki A.A., Irwin D.M., Graham L.C., Youson J.H.;
Al-Mahrouki A.A., Irwin D.M., Graham L.C., Youson J.H.;
Molecular clonding of preprintal nothers from several
osteoglossomorphs and a cyprintal nother several
Mol. Cell. Endocrinol. 174:54:58(2021).
-!- SUBCELUILAR LOCATION: SECRETER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/:GF/RELAXIN FAMILY.
EMBL: AF284408: AAK54684.1; --
HSSP; P01308: 11.NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AA; 12483 MW; 247CA4431376329F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 110 AA; 12343 MW; BDECCD7703E52E06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ADEYPYKDGGDJKVKRCIVEGCGGBPGNIFDJNOYDN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 -- ----EGSLQ-KRGIVEGCCISICSLYGDENYCN R6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1:1 AA
                                                                                                                                                                                                                                                                                                                    Interpro: IPRO04825: Ins/IGF/relax.
Pfam: PrC0049: Insuliu: 1.
SMARY: SR00277: INSULINS.
SMARY: SR003078: IGCF. I.
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Matches 44; Conservative
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Matches 48; Conservative
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                                                                                           SEQUENCE FROM N.A.
                                            NCBI_TaxID-54904;
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SEQUENCE
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Q98TBO
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27 QHLGGSHLVDALYLVCGPTGFFYNPK--RDVE------PLIGSLPPKSAQETEV 72
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                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota: Metazou: Chordata: Craniata: Vertcbrata: Euteleostomi:
Actinopteryqii: Neopteryqii: Teleostei; Ostariophysi: Cypriniformes:
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae: Catla.
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"A new cell secreting insulin.";
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Argenton F., Zecchin E., Bortolussi M.;

Farity appearance of pancreatic hormone-expressing cells in technic new, 87:217-221(1995).

SUBCELLOLAR LOCATION: SECRETED (BY SIMILARITY).

STRILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL. A1237750; CAC20109.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
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INSULIN B CHAIN.
INSULIN A CHAIN.
3195289E72AD6D25 CRC64;
                       O9DDE5;
01-MAR-2001 (1rEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
-------OKRGIVEOCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 ADFAFKUHAELIRKRGIVEQCCHKPCSIFELGNYCN 108
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Ol-DEC-2001 (TrEMBLrel, 19, Last sequ
Ol-MAR-2003 (TrEMBLrel, 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESIN; 203-GENE-980526-110; ins.
interPro; IPR064825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRIN'S; PR00277; INSULINB.
SMART; SM00078; IIGF; 1.
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11904 MW;
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                                                                                                                                         PRECIMINARY;
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53
168
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86
108 AA;
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Best Local Similarity
Watches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01308; 11.PH
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                                                                                                                                                                                                                                        Insulia precursor.
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us-09-423-100-4.rspt

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27 QHI.CGSHI.VDAI.XI.VGGPTGFFYNPK--KDVDFL-IGFLPPKSGP-ENEVADFAFKDHAE
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01-53N-2001 (Triminal 17, Last sequence update)
01-53N-2001 (Triminal 17, Last sequence update)
01-MmAr=2003 (Triminal 12, Last annotation update)
Proposition (Fragment).
Ambioplites rupestris (Rock bass).
Entaryota, Metazoa: Chordata, Craniata, Vertebrata; Enteleostomi,
Actinoplerygii, Meoplerygii, Teleostei; Enteleostei; Nectoleostei,
Acanthomorpha, Acanthopterygii: Percomorpha; Perciformes; Percoidei,
Centrarchidae: Ambiopiites.
                                                                                                                                                                                                                                       Catestomus commersoni (White sucker).
Eukaryota, Metazoa, Chordata, Cramiata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
Catestomidae, Catestomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Al-Mahrouki A.A., Irwin D.M., Youson C.H.;
"Molecular clocking of preprointsulin club.";
Submitted (OCT-1999, to the EMBL,GeorBank/DDBJ databases.
--- SURCELLULAR JOCATION: SECRETED (HY SIMILARITY).
--- STATLARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
HSSP; PC1308: 1LPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.4%; Score 205.5; DB 13; Length 108; 50.0%; Pred. No. 1.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X MEDIANE_21203557; Pubmed :1306;71;
A H-Mahrouki A.A., Irwin D.M., Graham :.C., Youson J.H.;
All-Mahrouki A.A., Irwin D.M., Graham :.C., Youson J.H.;
"Molocular closing of proproinsulis cDNAs from several
r ostcoglossomerphs and a cyptinid";
Kol, Cell. Endocrinol. 174:51-58(2001).
... SHORELIGIAR :JOANTION: SECRETED (BY SIMILARITY).
... SHORELIGIAR :JOANTION: SECRETED (BY SIMILARITY).
R - SHORELIGIAR :JOANTION: SECRETED (BY SIMILARITY).
R - SIMILARITY: FRECNES TO THE :INSULIN/:GF/RELAXIN FAMILY.
E- SIMILARITY: FRECNES TO THE :INSULIN/:GF/RELAXIN FAMILY.
R - INCOPTOR: IPROUGHS: Ins/:GF/relax.
R - Pfam: PP00049: Insulin: 1.
R - PROSITE: PROUGHS: INSULIN: 1.
R - ROSITE: PROUGHS: INSULIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11873 MW: E425310696FBAFC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10100 MW; E86C8B256DC69D39 CRC64;
                                                   01-70N-2001 (TrEMBLRG), 37, Created)
01-70N-2001 (TrEMBLRG), 17, Last sequence update)
01-MAR-2003 (TrEMBLRG), 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LiterPro; IPRO04825: Ins/IGF/relax.
Ptam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                        Preproissulin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECTIONCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-7971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 OHLOGSHIVEALYIVGGERGFFYTFKTRFENEULOVGOVELDOGPGADSLOPGADFOSH (1)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 27, Last annotation epdate)
Preproficeusin (Fragment).
Buathonemus petersi.
Bukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostemi:
Actioopterygii: Neopterygii: Teleoste: Osteoglossomorpha;
Osteoglossiformes: Mormyr.dae: Gnathonemus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5% Score 212.5; DH 13: Longth 109; 44.8% Pred. No. 1.9e-17; Uve 12: Mismatches 14; infols 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21203577 Pubmed-11366171;
Al-Mahrouki A.A., Irwin D M., Graham L.C., Youson J.E.;
Molecular cloning of prepriorinsulin cobhas from severa;
osteoglossemorphs and a cyptinid";
Mol. Cell. Endocrinol. 174:51-56(201).
T. SHECELLUIAR (CCATION: SECRETE) (BY SIMILARITY).
T. SHECELLUIAR (CCATION: SECRETE) (BY SIMILARITY).
RARLS ARIB9587; ARX28711...
RISSP: P01306: 14:58.
TIPED-PO: TEPEJ-9587; TO THE INSCLIN/TGF/RELAXIN FAMILY.
RISSP: P01306: 14:58.
TIPEJ-PO: TEPEJ-9587; TO THE STORY SECRETES (BY SIMILARITY).
RISSP: P01306: 14:58.
TIPEJ-PO: TEPEJ-9687; TO THE STORY SECRETES (BY SIMILARITY).
SMART; SMG0076: 11GF: 1.
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Submitted (AFR-2001) to the EMBL/Genbank/shal databases.
+!- SUBCELLUTAR LOCATION: SECRETES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/16F/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                  | DOCUMENT | PRODUCT | DESCRIPTION | DESCRIP
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HSSP: P01308; 11NP.
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Best Local Similarity
Matches 43: Conserv
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Gaps

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Best Local Similarity 46.7%, Fred, No. 1.84-16;
Matches 42; Conservative 13; Mismatches 26; Indels
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GPUNIE S		ABBAFK 6.
CVELGGGPGA-GSL	=	CALIGRAPPOSENEV
QHLOGSHLVEALYLVGGERGFFYTPKTRREAEDLO++ VGUVELGGGRGA+GSLQPUALR B9		HECGSHEVERALYEVCGORGFFYNPK - ROVOPEMGFEPPRAHGAAAAPGGENEVA
QHUCGSHLVEALYLVC		QHECGSHIVEALYLVC

Cy Dp qq c_{Y}

Search completed: September 15, 2003, 12:03:29 Job time : 35.5986 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuges 2.00.
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OM protein - protein search, using sw mode

September 15, 2(0), 11:44:15 | Search time 36:5339 Seconds (without ablanments) 225:342 Million cell updates/sec Run on:

US-09-423-100-5

TO THE PROPERTY OF THE BUYER 294 1 FVNQHLOGSHLVEALYLVOG. Perfect score: Sedneuce:

BLOSUM62 Sccring table:

1:07863 seqs, 158726573 residues Gapop 10.0 , Sarext 0.5 Searched:

Total number of hits satisfying chosen parameters: length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Listing first 45 summaries Post-processing: Minimum Naton 1% Maximum Natoh 100%

Database

| SIDS_/gcgdata/geneseq/geneseqp.cmb! /AA1980.DAT:
| SIDS_/gcgdata/geneseqy.cmb! /AA1980.DAT:
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| SIDS_/gcgdata/geneseqy.cmb./AA1987.DAT:
| SIDS_/gcgdata/geneseqy.cmb./AA1997.DAT:
| SIDS_/gcgdata/gen /SIDS1/gegdata/geneseg/genesegp-embl/Aa2600.0400 /SIDS1/gegdata/geneseg/genesegp-embl/Aa2600.0400 /SIDS1/gegdata/geneseg/genesegp-empl/AA2002.0400 /SIDS1/qcqcata/geneses/genese.pr-emb1/AA2003.DAT A_Geneseq_19Jur03:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		resertiblish	Homan insuling pro-	Biman ord-insulls	Protestine / entend	TO THE CAR DELTH	Ellian oro-insula	Fusion profein con	hCS misi protestli	SOP-projestin hyb	Mating factor alph
		IL:	AAY42859	AAR6890;	AAR78665	AAR68900	AAR68899	AAR78662	AAY42860	AAR98897	AAR71692
		23	20	S.	ij	-	 T	16	56	17	÷
		Match Length DB ID	52	56	95	63	96	96	107	116	137
œ,	Ouery	Match	300.0	100.0	100.0	100.0	100.0	150.0	100.0	100.C	100.0
		Score	294	294	294	\$ 62	294	294	294	294	294
	Result	No.	7	2	m	4	Š	9	7	œ	б

Mating factor alph Mating factor alph Chimeric arctain	Proinsulin analogu Example of buman i	Di-Arg-(B31-32)-Hu	Insi double-chain Glycosylphosphatid	SOD-proinsulin hyb	Human proinsulin a	Himan mature insul	Human insulin. Ho	Ε	Modified pJB59 mod	Single chain insul	Met-Arg-Met-single		pKV142 modified in	Sequence of novel	Gly-A21-di-Arg-(B3	Preproinsulin 1.	Ins 4 double-chain	Ins2 double-chain	Example of human i	pAK679 modified in	Modified Human ins	Amino acid sequenc	Sequence encoded b	pJB5	Modified pdB59 mod	pJB5	E	peptide/l	Ξ.	YAP3 signal peptid
AAR71694 AAR71695 AAV4286:	735	AAR65883	AAW18007 AAR79056	AAR98895	AAP20002	AAB12//-	AAM48219	AARS6046	AAR96050	AAW06807	AAW06809	AAW06810	AAR87086	AAP62132	AAR65882	AAW47365	AAW17999	AAW17998	AAR11898	AAR87085	AAY28341	AAB30704	AAP71019	AAR96047	04	20	318	317	N	AAR88181
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ALIGNMENTS

Insulin: precursor: growth hormone; chaperone: intramolecular; folding: conformation: chimeric protein; cleavable; recombinant; Human insulin precursor, SEQ ID 5. AAY42859 standard; protein; 52 AA (first entry) .9-JAN-2000 AAY42859; RESULT 1 AAY42859

production; yield

Homo sapiens

W09950302-A1 07-0011-1999. 38WC-CN00052 98WO-CN00052 31 - MAR-1998; 31-MAR-1998; (TONS-) TONGHUA GANTECH BIOTECHNOLOGY LTD.

WPI; 1999-610839/52.

New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin $^{-}$

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 · FEB - 1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                       Segmence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pept.ide
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AAR78665
     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a numan insulin precursor comprising insuling A and B chains. This insuling precursor is a remponent of the chimneric proteins b5d-mini-precised; (AAY42860) and the chimner protein given in AAA42861. These chimners proteins additionally contain an Niterminal fragment of huma; growth beamone (h6H) and a cleavable of peptide linker (AAY42867). The h6H pertion of the chimneric protein acts as an intramolecular chaptering (hCM) for the insulin preciser.

The mabling it to fold correctly. The cleavable peptide linker has a crimnal Arg residue which enables the h6H portion of the chimner protein to be removed after including horting of the chimner protein to be removed after including the protein can be provide human insulin with organization chimneric protein and provide human insulin with sorrectly linked estable bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a micropreparism host, but also processed the fisher and recreases the sinterrollar the solutility of the fusion protein and decreases the interrollar four annotation and decreases the interrollar interrollar annotation and decreases the interrollar interrollar annotation and decreases the interrollar interrollars and not the folding of the fusion protein and decreases the interrollar interrollars and not an annotation and decreases the interrollar interrollars and not an annotation and not annotation and not an annotation and not annotation an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the fusion proteins, thus allowing folding of the fused institu precursor at commercially useful high concentrations. The procedural steps of cyanogen bromide cleavage, oxidative suiphitotysis and related purification steps can thus be eliminated, along with the use of tiah concentrations of mercaptan or the use of hydrophotic absorper, 1981.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FUNCHIGGSHLUMBALVLOGGREGHTPKTRATVEGOCTSTOSLYGJENYDK 52 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 114 | 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 294: DP 20: Length 52: Pred. No. 1.60-26: 0: Indels of Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B-chain: C-chain; disciphide; agent.
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                         Claim 12; Page 29 30; 46pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ludwig J, Obermeier R,
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100.0%
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nes 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mercaptan; chaptropic
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\mathbf{x} (\mathbf{x}, \mathbf{x}, \mathbf{y}) (\mathbf{y}, \mathbf{x}, \mathbf{y}) (\mathbf{y}, \mathbf{x}, \mathbf{y}) (\mathbf{y}, \mathbf{x}, \mathbf{y}) (\mathbf{y}, \mathbf{x}, \mathbf{y}, \mathbf{y})
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Freedmanth is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in presence of a chaotropic agent and in aq. medium of pH 10-11, treating the prou. with 3-0 q hydrophobic adsorber resin per 1 aq. medium of pH 4-7, isolating the adsorbed resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with known methods 1. Involves fewer stages (esp. no sulphitolysis or cyanogen bromide cleavage) and overall losses during purification are reduced, i.e. the process is quicker and gives better yields. Sequences of insulin chain A, B and C are given in AAR68895-97. Sequences of insulin chain A, B and C are given in AAR68899-901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 FVNQHEGGSHEVEALYEVGGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 294; DB 15;
100.0%; Pred. No. 1.7e-26;
iive 0; Mismatches 0;
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/label= Giy-(A2-A20)-R3
/note= "human insulin A-chain"
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/rote- "buman insulin B-chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Socation/Oualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Profesuilo seguence 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-284754/38
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Gaps

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indels

Sednence

Length 63;

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Pro-insulth is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SE residues per Cys residue, in presence of a chaotropic agent and in ag. medium of pH 10-11, creating the prod. with 3-50 g hydrophobic adsorber resin per I ag. medium of pH 4-7, isolating the adsorbed resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with contectly bonded Cys bridges. Compared with known methods it includes fewer stages (esp. no sulphitolysis or gamogen bromide cleavage) and overall losses during purification are reduced, i.e. the process is quicker and gives better yields. Sequences of insulin chain A, B and C are given in AAR68898-97. Sequences of pro-insulin l4 are given in AAR68898-901.
   involves fewer stages (esp. no sulphitolysis or cyanogen bromide cleavage) and overall losses during purification are reduced, i.e. the process is quicker and gives better yields. Sequences of insulin chain A, B and C are given in AAR68895-97. Sequences of promingulant 1-4 are given in AAR68898-901. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVNOHIGGSHLVEALYLVGGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 FVNQHIGGSHIVEACYLVGGERGFFYTPKTRGIVEGCCTSICSLYQLENYCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodm. of pro-insulin with correct dissulphide bridges - by treating recombinant precursor protein with mercaptan in alkali and in presence of chaotropic agent, then isolation on hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B chain; C.chain; disulphide;
                                                                                                                                                                                                                                                                                                                          100.0%; Score 294; DB 15; 100.0%; Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 294; DB 15;
Pred. No. 2.9c-26;
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sabel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 11: 15pp: German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR68899 standard; peptide; 96 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first_entry)
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pro-insulin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-177718/22.
                                                                                                                                                                                                                                                                                                                                                       Restinceal Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP600372-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR68899;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                             Cuery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR68833
          888888%%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an example of a proinstlin molecule corresp. Of the degeneral formula R2-R1-(B2-R29)-Y.X.61y-(A2-A20)-R3 (11), 10 formula (11), X = Lys, Arg or a peptide of 2-P6 amino acids cong. Lys or Arg at the N- and C-terminis Y + a natural amino acids R2 - B, Arg. Lys, a peptide of 2-P6 amino acids Confg. Phe or a bond: R2 - B, Arg. Lys, a peptide of 2-45 amino acids confg. Arg or Lys at the N- and C-terminis R3 - a natural amino acids confg. Arg or Lys at the N- and C-terminis R3 - a natural amino acids confg. (A2-A20) and (B2-B2)) are the insulin A- and B-CB41, sequence of From human or chlor insulin. The prointsulin The reaction resolution of mercapisan per Cys residue of prolitation. The reaction takes place in the presence of a chootropic axillary agent at PH 10-11 and results in prointsulin with correctly likes upstines bridges. Reaction with trypism and opt. Confrex/Poptidase B victor B victor with trypism and opt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000 NO. 100 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro-insulin is produced by treating recombinant procusor profets, which a mercaptan to provide 2.16 SH rossdaces per 1987 residies, in presence of a chactropic agent and in aq. medium of ps 10-11, treating the prod. with 3-50 q hydrophobic adsarder resin per Lagrandium of ph 4-7. Asolating the adsorbed resin and pro-insuling the adsorbed resin and pro-insuling the medium of pro-insuling this method produces pro-insuling with correctly bonded Cys bridges. Compared with known methods in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PVNQHLGGSHLVEALYLVGJERGFFYTPKTRGTVEGOTFSTOSLYGLENYGN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Produced pro-insulin with correct disulphide bridges by treating recombinant precursor protein with mercaptan in alkal, and in presence of chaoticpic agent, then isolation on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Longth 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro-insulin; A-chain; B-chain; C-chain; disulphide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 294; Ob 16:
Pred. No. 1.7e-26;
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Example 2; Page 13; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR68900 standard; peptide; 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chermeier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mercaptan; chactropic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93EP-0118993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.0
Matches 52, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pro-insulis 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydrophobic resin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerl M, Ludwig J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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02-MAR-1995
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AAR68900;

AAR58900 RESULT

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Length 96;

Length 95;

100.0%; Score 294: DB 16; 100.0%; Pred. No. 2.9e-25;

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Local Similarity 100.
es 52; Conservative
96 AA;
                                                                                                19-JAN-2000
                                                                                                                                                                          07-0CT-1999.
                                                                                                                                             Synthetic
                                                                                     AAY42860;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
conarbos
           Colery March
                                                                                                                                                                                                                       Gan 2;
                 Bos: Loc
Matches
                                                              RESULT 7
                                                                    5.2.4.2.360
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1.
                                                                                                                                                                                                                                                                                   Isolation of insulin that is correctly post-translationally processed - by reacting profiles with a mercaptan in the presence of a chaotropic agent and purifice, after absorption to hydrophobic
                                                                                             Profestine post-translational modification, recombinant production: protein folding: conformation.
           1 PVNQHLOSSHLVBALYLVCGERGFPYTPKTRGIVEQCCTSLCSLYQCBNYCN 5/
                 indels
                                                                                                                                             "a peptide of 4 amino acids"
÷.
                                                                                                                                                                                   /label- 61y (A2-A20)-F3
/mote= "forma insulia Archain"
                                                                                                                                                       /label= R1-(82-529).r
/note= "human insulic B-chain"
                                                                                     Fusion protein contq. proinsulin sequence 3.
Mismatches
                                                                                                                                                                                                                                                              Same | W.
                                                                                                                            Location/Qualifiers
                                                   Ę
                                                                                                                                                                                                                                                              Obermeier R,
                                                                                                                                                                                                                                                                                                                Example 2: Page 8: 16pp: German.
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                                                  AAR78662 standard: protein; 96
                                                                                                                                                                                                                            958P-0101748
                                                                                                                                                                                                                                       94DE-4405179.
                                                                                                                                  41..44
/labe:= R2
                                                                                                                                                                        /label + X
76...96
                                                                         (first entry)
Conservative
                                                                                                                                             /note-
                                                                                                                                                                                                                                                              Ludwig 3,
                                                                                                                                                                                                                                                                         WPI; 1995-284754/39
                                                                                                                                                                                                                                                                                                                                                                                                                  hydrophobic resin
                                                                                                                                                                                                                                                   (FARH ) HOECHST AG.
                                                                                                                                                                                                                            09-FEB-1995;
                                                                                                                                                                                                                                       18-FEB-1994;
                                                                                                                                                                                                                23-AUG-1995.
52;
                                                                         03-APR-1996
                                                                                                                                                                                                     EP668292-A2
                                                                                                                Synthetic.
                                                             AAR78562:
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                                                                                                                                                                               Peptide
                                                                                                                                                  Popt:de
                                                                                                                                  Region
                                                                                                                                                                   Region
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Matches
                                                                                                                            Key
                                       RESULT 6
                                            AAR78662
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This sequence represents a chimeric protein, hGH-mini-proinsulin.
This chimeric protein contains an N-terminal fragment of human growth horzone (hGH) of the sequence given in AAV42855, a cleavable peptide linker (AAV42857), and a human insulin precursor comprising insulin as an intramplendar chaperone (HMC) for the chimeric protein acts as an intramplendar chaperone (HMC) for the chimeric protein acts and intramplendar chaperone (HMC) for the insulin precursor, enabling it to fold correctly. The cleavable peptide linker has a content of protein to be removed after folding has taken piece. Production of the chimeric protein to be removed after folding has taken piece. Production of recombinant human insulin via an hGH-proinsulin chimeric protein can provide human insulin via an hGH-proinsulin chimeric protein can provide human insulin via an hGH-proinsulin prides with chemen insulin. The IMC sequences not only protect insulin sequences to human insulin. The IMC sequences not only protect insulin sequences of human insulin. The IMC sequences not only protect insulin sequences the fusion protein and decrease the intermolecular interactions among the tusion proteins, thus allowing folding of the fosed insulin precursor at commercially useful high concentrations. The procedural steps of
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin {}^{\circ}
                                                                                                                 1 FVNQHLOGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSFYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin, precursor, growth hormone, chaperone, intramolecular; folding; conformation; chimeric protein; cleavable; recombinant;
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyanogen bromide cleavage, oxidative sulphitolysis and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 294; DB 20;
Pred. No. 3.2e-26;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hGH-mini-proinsulin chimeric protein.
                                                                                                                                                                                                                                                                                                                                                     Y.
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                                                                                                                                                                                                                                                                                                                                                     AAY42860 standard; protein: 107
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100.08;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production; yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 - MAR - 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09950302-A1
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Matches

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RESCLT 8 AAR98897

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ArgB11. AgB31 comprises the B and A chains of a claimed human insulin derivative. In the final claimed compsn. they are covalently connected via disulphide bonds between Cys residues A7/B7 and A20/R19. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for diabetes. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ86425 encodes AAR71692 mating factor alpha 1-Insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mating factor alpha 1-Insulin precursor ArgBl, ArgB31 N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 294; DB 16; Longth 137; 100.0%; Prod. No. 4.1e-26; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                          Human insulin precursor ArgB31; diabetes; Zinc ion complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acylated insulin deriv, which may be present as a Zinc ion complex - is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jonassen 1;
                                                                                                                                                                                                       Mating factor alpha 1-Insulin precursor ArgB31
                                                                                                                                                                                                                                                                                                                                                                                                                                    1.85
/label- mating factor alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halstrom JB, Havelund S,
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 78; 100pp; English.
     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR71694 standard; Protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66..16
/label - R-chain
117..37
/label - A-chain
AAR71692 standard: Protein; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93DK-6001044.
9409-6190829.
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                                                                                                                 (updated)
(first entry)
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nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
                                                                                                                                                                                                                                                                                           alpha î.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSUB; AAQ86425
                                                                                                                                                                                                                                                                                              mating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1993;
62-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO9507331-A1
                                                                                                                                                                                                                                                                                                                                                   Horro sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Markussen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
20-NOV-1995
                                                                                                                 25-MAR-2003
20-NCV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                           AAR71692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coory Match
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matiches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR71694
     FEXAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises folding a hybrid polypeptide comprising proluctions that permit correct disulphide bend formation and conditions that permit correct disulphide bend formation and conditions that folded protein to enzymath of drawage. The insulin produced can then be purified. This sequence is a SOD insulin of chair Arg-insulin A chain hybrid polypeptide and is encoded by the plasmid construct pubsist. Transformation of the propert of E.coli host ceals with pubsist. TAT pransformation of the propert expression of the properties and construct pubsision of the properties. The method produces recombinant numan misulin conduction. The method produces recombinant numan misulin production. The method produces recombinant numan misulin production to adult dominant numan misulin procedures involving cyanogen bromide and sulphinolysis to protect procedures involving cyanogen bromide and sulphinolysis to protect efficiently to the native structure even with the leader attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
     Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant insulin prodm. by correctly folding pro-insulin hybrid polypeptide - then enzymatic eleavage of folded product, does not require sulphite protection of SH nor use of cyanogen bromide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11: 111: 111: 111: 1111: 1111 | 1111 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
                                                           1 FVNCHLCGSHJVBALYJVCGERGFFYTPKTRGIVECCTSTCSLYJLENYDK %2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        new method for the production of recombinant human insulin
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enzymatic cleavagos cyanogen bromidos sulpolitolysis.
  STABIL
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; Pred, No. 3.5e-26;
C; Mismatches G;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BICT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1B; Figure 7; 69pp; English.
                                                                                                                                                                                                                                                             AAR98897 standard; Protein: li6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOD-proinsulin hybrid polypeptide.
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Best Local Similarity 166.0%;
Matches 52; Conservative 0.
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952A-0000142.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Cys unprotected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9620724-A1.
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10-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                           63 - PER- 1997
52;
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Acylated insulin deriv, which may be present as a Zinc ion complex - is used to treat diabetes and is rapid acting.
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                                    1..85
/label- mating factor alpha l
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 85; 100pp; English.
                                                                                       95..125
/label- B-chain
                                                                                                                    126..146
/label- A-chain
                                                                                                                                                                                                                                         93DK-0001044.
94US-0190829.
                                                                                                                                                                                                                94WO-DK00347
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                                                                                                                                                                                                                                                                                                           Halstrom JB,
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EFSt.iocal Similarity TUC...
FFSt.iocal Similarity TUC...
These 52: Conservative
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N-PSDB; AAQ86432.
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Home sapiers.
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Markussen J;
                                                                                                                                                           W09507931-A1
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                                                                                                                                                                                                                16-SEP-1994;
                                                                                                                                                                                                                                            17-SEP-1993;
                                                                                                                                                                                                                                                       32-FEB-1994;
                                                                                                                                                                                     23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                          Key
Protein
                                                                 Pept.ide
                                                                                           Peptide
                                                                                                                     Pepride
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           Human insulin procursor ArnBl, Arga31: diabetes: Sinc ion encplex:
mating factor alpha i) N-terminal ESAFAEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human insulin precursor ArgB1, ArgB31; diabetes; Zinc Lon complex; mating factor alpha 1; N-terminal EEAEAEAER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mating factor alpha 1-Insulin precursor ArgBl, ArgBl N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          j.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 294; LB 16; Longth 135; 100.0%; Prod. No. 4.46+26;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Acylated insulin deriv. Which may be present as a Zinc ion complex - is used to treat diabetes and is rapid acting.
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                                                                                                       /label- mating factor alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                               /label+ N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                Haveland S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5: Pages 82-83; 160pp; English
                                                                            Location/Qualifiers
1..85
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                                                                                                                                              94..124
/labeir_B-chain
                                                                                                                                                                     125..145
/label= A-chain
                                                                                                                                                                                                                                                                    94WO-DK00347.
                                                                                                                                                                                                                                                                                            93DK-0001044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 52: Conservative
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N-PSDB; AAQ86429.
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                                                                                                                                                                                                                                                                                                                                                              Andersen AS,
                                                  Homo sapiens
                                                                                                                                                                                                                W09507931-A1
                                                                                                                                                                                                                                                                    16-SEP-1994;
                                                                                                                                                                                                                                                                                                          02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1995
                                                                                                                                                                                                                                                                                             17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                             Karkussen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                         23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR71695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes
                                                                             Key
Protei::
                                                                                                                                             Peptide
                                                                                                                    Peptide
                                                                                                                                                                        Peptide
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AAQ86432 encodes AAR71695 mating factor alpha 1-Insulin precursor ArgB1, ArgB31 N-terminal EEAEABAER. The insulin precursor comprises the 3 and A chains of a claimed human insulin derivative preceded by the N-terminal amino acids EEAEABAER. In the final claimed composition are covalently connected via disulphide bonds between Cys residues A7/B7 and A20/B19. The derivative, which may be present dispetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulia; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 294; DB 16; Length 146; 100.0%; Pred, No. 4.4e-26; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42861 standard; protein: 150 AA
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Anmerer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR11899 standard; Protein: 52 AA.
                                                                                                                                                        Uhlmann E,
                                                                                                                                                                                                                                                        Disclosure; Page 2: 2pp: German.
                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90EP-0121887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84DK-0002665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85DK-0030582
                                                                                                         89DE-3927449
                                                                      89EP-0120056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              51; Conservative
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Norris K, Voigt HO;
                                                                                                                                                        Koller KP, Riess GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO-NORDISK
                                                                                                                                                                               WPI; 1990-141149/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                 (FARH ) ROECHST AG.
                                                                                                                                                                                                                                                                                                                                                                              57 AA;
                                                                                                                                                                                             N-PSDB: AAQ04335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Home subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
22-JJL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3C-MAY-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-1985;
                                                                                                         19-AUG-1989:
                                                                      28-OCT 1989;
                                                                                             33-NOV-1988;
                                               09-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP427296-A.
                      EP367163-A.
                                                                                                                                                                                                                                                                                                                                                                                Segrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR11899;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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This sequence represents a chimeric protein, which contains an N-terminal fragment of human qrowth hormone (1971) of the sequence qives in AAV42856, a cleavable peptide take (AAV42857), and a human lessils precursor comprising insulin A and B chaims (AAV42859). The hortion of the chimeric protein arts as an intracolemiar dispersor (INC) for the insulin precursor, enabling it to Gild correctly. The representation of the chimeric protein arts as an intracolemiar dispersor (INC) for the insulin precursor, enabling it to Gild correctly. The representation of the chimeric protein to be removed affor indicate his taken please. The chimeric protein to be removed affor indicate his taken provide fummer insulin via an heighprotissuile chimeric protein can provide fummer insulin with fewer necessary procedural steps, and better resulting a lighter yield of human issulin. The INC sequences not only protect issuling sequences from intracellular degradation by a riceobratism host, but also promote the folding of the lusson proteins, and decrease the intermolemular interactions among the fusion proteins, thus allowing folding of the fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                              procedural steps of eyanogen bromide cleavage, exidative sulphinallysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /imbel-Lys residue linking masanin B chain to A chain
1.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proinsulin analogue with a Lys residue linking the A and B chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New chimeric proteins containing human great: however fragment, particularly for the production of homen issuing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin fusion protein; pre-insulin analoque; tendamistate:
Lys-Lys bridge: ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       indels
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                                                                                  (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label Insulin B chain 37..57
                                                                                                                                                                                             Claim 14) Page 30-31; 46pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR04582 standard; protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
                                   98WO-CN00052
                                                           98WO-CN00052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                   WPI; 1999 610839/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 AA;
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14-SEP-1990
                                   31-MAR-1998;
          07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR04582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
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                                                                                                           San 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
AAR04582
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This sequence is joined to the Ofterminus of an Noterminal fragment comprising opt. modified tendamistate. This fusion protein ray be converted into busan insulin using known methods. The synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 FVNQHLCGSHIVEALYLVCGERGFFYTPKTKGIVEOCTSICSLYQLENYCN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insulin fusion proteins comprise pro-insulin analogue linked to tendamistate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 57:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 291: DB il:
Pred. No. 3.8e-26;
l; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quoc was prepared by the phosphoramidite method. See also AAG04336.
                                                                                                                                                                                                                                                                                                                                                                                      Wallmeier H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human insulin; diabetes: transpeptidation.
/label- insulin A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example of human insulin precursor.
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Thim L;

Hansen MT,

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Search completed: September 15, 2003, 12:00:59 Job time: 37.5305 secs
55555×8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human insuling recombinant productions amorphouse memospherinal form; diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is a specific example of an insulin derivative which can be obtained in amorphous, monospherical form by dissolving in an n-propanol/Duffer mixture (pH 4.5-6.5) having n-propanol content 15% relative to water. The solution is then diluted with water to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amorphous, mono-spherical form of insulin derivs. - for treating diabetes mellitus, are produced by diluting soln. in aq. isopropanol, are stable when dried or in suspension
                                                                              This human insulin procursor has correctly positioned disciplide bridges between the A and B chains and is more resistant to proteolytic digestion than prior art insulin precursors. Yeast, strains transformed with LNA encoding this precursor can be cultured to secrete it in high yields. The precursor can be converted into mature numan insulin by transpeptication. See also AARIB97-98.
(Updated on 25-MAR-2003 to correct PF Field.)
                                                                                                                                                                                                                                                                                                            1 FVNQHLGGSHLVEALYLVGGERGFFYTPKTRGIVEQCCISTCSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                             1 FVNQHEGGSBEVEALVERENGGERGFFYTPKSKGIVEGCCTSICSLYQUENYCN 52
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           Human insulia precursors - expressed with corperty positioned
dissulphide bridges giving improved resistance to proceedisty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Di-Arg-(851-32)-Human insulin amorphous, monospherical deriv.
                                                                                                                                                                                                                                                        Length 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli).
                                                                                                                                                                                                                                                                                 stapu:
                                                                                                                                                                                                                                                    Score 287; 38 12;
Pred. No. 9.8e-26;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (produced recombinantly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label⇒ insulin_B-chain
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/label- insulio_A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qual::iers
                                                                                                                                                                                                                                                                                                                                                                                                             AAR65883 standard; protein; 53 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2: Page 5: 10pp; German.
                                                       Claim 3: page 18: 28pp; English.
                                                                                                                                                                                                                                                        97.68:
95.28:
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(iirst entry)
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.2
Matches 50, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARE ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deil P, Geisen K,
                                                                                                                                                                                                                             52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1994;
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26-JUN-1995
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                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR65883;
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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1; Gaps
reduce a propagol content to below 15%. The resulting insuling proparation is stable and can be used for the treatment of diabetes mellitus.
                                                                                                                                                                                                                   DB 15; Length 53;
                                                                                                                                                                                Indels
                                                                                                                                     th 96.4%; Score 283.5; DB 15; Similarity 98.1%; Pred. No. 2.56-25; 52; Conservative 0; Mismatches 0;
                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                    S.3 AA;
                                                                                                                                         Query Match
Sest Local S.
Matches 52
                                                                                                        Seguence
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compuget Ltd.

- protein search, using swindel OM protein September 15, 2309, 21:57:40 ; Search time 11:9283 Seconds (without alignments)
[84:449 Million cell quartez/sec Run on:

US-09-423-100-5 294 1 FVNQHLGGSHLVEALXLVGG..........IVKQCGTSIGSLYJLENYGK Title: Perfect score:

Sequence:

328717 seqs, 42316858 residues Searched:

Gapop 10.0 / Gapext 0.5

BLCSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000600000

Post-processing: Minimum Match 1868 Maximum Match 1868 Listing first 15 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result beam printed, and is derived by analysis of the total score distribution.

APPLICANT: Lodwig, Jurgen
APPLICANT: Lodwig, Jurgen
APPLICANT: Sabe), Walter
TITLE OF INVENTION: Process For Obtaining Proinsulin
TITLE OF INVENTION: Possessing Correctly Linked
ITTLE OF SQUENCES:
TOWNSER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth A. Genoni, Esq.
STREET: Rt. 202-206 No. 5473649th/P.O. Box 2500
GILY: Somewyille

DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT STATE: New Jersey CCUNIRY: U.S.A. ZIP: 08876-1258

COMPUTER: DISTRIBUTED S.O. INCH., 1.94 PM.
COMPUTER: DISTRIBUTED S.O. INCH., 1.94 PM.
SCHWARE: WARDERFEET S.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,376A
FILING DATE: December 1, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/160,376A
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: BALDATA V. MOLTER: ESG.
REGISTRATION NUMBER: 31,287
REFERENCE/NOCKET NUMBER: 106: 92/F 384
FERENCE/NOCKET NUMBER: 106: 92/F 384
FERENCE/NOCKET NUMBER: 106: 92/F 384

TELEPHONE: (90H) 231-4079
TPELEFAX: (90H) 231-2255
INFORMATION FOR SEC 15 NO: 7: SEQUENCE CHARACTERISTICS:

56 Amino Acids

not relevant

TYPE: Amino Acid (AA) TOPOLOGY: not relevan

		æ			SUMMARIES		
Result No.	Score	Query Match	Query Match Length	23	(2)	Description	
-	294	100.0	56	-	US-08-160-376A-7	Sequence 7. April	
12	294	10C.0	95	-	105-03-389-487-31		
m	294	100.0		-	US-08-160-376A-6	9	
4	294	100.0		7	US-08-291-06CB-5	S.	
ហ	294	100.0		٦	US-08-160-376A-5	S,	
9	294	100.0	96	٦	US-08-389-487-8	∞,	
7	294	190.0	137	7	US-08-400-256-39	39.	
ഡ	294	100.0	137	~	US-08-975-365-39	~	
6	294	130.0	145	-	US-08-400-256-45	45,	
10	294	150.0		~	118-08-975-365-45	45,	
1	294	150.0			08-08-400-256-48	8	
12	294	100.0		~	US-08-975-365-48	α ~*	
13	162	0.65		-	US-08-030-7318-44	 	
14	283.5	96.4	\$ \$	-	05-08-2/3-617-4	-,	
15	283.5	96.4		٠,	US-08-981-988A:42	Sequence 42, April	
16	278.5	94.7	. ۲ ک	77	US-09-477-924-3	, r	
17	278.5	94.7	ir	-,*	08-09-723-981-3	٠,٠	
18	278.5	94.7	I.	••	05-09-723-896-3		
19	277.5	4.46	5.3	-	US-08-233-617-3	Sequence of Applit	
20	277	94.2	đ.	m	US-08:900-574-3		
21	276.5	94.0		~ 1	US-08-900-574-6	ني	
22	276.5	94.0	99	(L)	US-08-900-574-5	ر.	
23	276.5	94.0		٠,	0S-08-981-988A-1	, :	
24	276.5	0.46		~1	US-08-981-986A·5	J	
25	276	93.9	67	~	US-08-900-574-7	r·.	
26	275.5	93.7	ic.	~.	US-09-261-853-2	ci	
27	275.5	53.7	65	~	US 08-468-6746-71	Ē	

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Gaps

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Indels

Length 56,

100.0%; Score 294; DB 1; 100.0%; Pred. No. 4.9e-29; ative 0; Mismatches 0;

Obery Match Best Local Similarity 100. Matches 52, Conservative

28 275	is.	93.7	55	1	US-08-780-571-71	
23	ν. Vi	53.7	88	٦	US-08-468-6743-41	41,
27	5.5	93.7	68	. 1	US-08-78C-571-41	41,
2.7	5.5	93.7	91	-1	US-08-468-674B-45	45
3.2 275	10.	63.7	91	- 1	US-08-78C-571-45	, 12
27	in.	93.7	104	~	US-08-400-255-15	
2.3	in.	93.7	104	~	US-08-975-365-15	.5
3.5 27.5	in.	93.7	117	٣	US-09-012-669F-37	37
	ر در	93.7	124	_	US-08-446-646-3	3,
	5.5	53.7	124	m	US-09-012-669F-36	Sequence 36, Appl
38 275.5	ις.	93.7	138	m	US-08-932-082-19	19
3.9 27.5	ις.	7.66	14 C	-	US-08-400-256-33	
	5.5	93.7	140	-	CS-08-400-255-42	42.
	5.5	63.7	140	(F:	CS-08-975-365-33	33,
42 27	ري د د	93.7	140	m	US-08-975-365-42	42,
	5. .S	r.	67	•3	US-08-981-988A-2	2, 4
	ω. 2	(3	S	er:	US-08-900-574-4	4
45 272	2.3	65.3	50	4	US-08-981-988A-4	4
					ALIGNMENTS	
RESULT 1						
JS-08-160-376A-7	7. A-7	(
. Sequence 7, Application US/08150376A	7. A.E.	oplicati	co US/I	081	50376A	
; Patent No. 5473049	547	73049				
: GENERAL INFORMATION:	INFO	RMATIONS				
: APPLICANT:	FNE	Cherme	Obermeier, Ranier	an i	เม	
: APPLICANT:	NT:	Gerl,	Gerl, Martin			

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APPERSSEE: Kenneth A. Genozi, Esq., STREET: Rt. 202-206 No. 5473649th/P.O. Box 2500
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barbara V. Mairer, Esq. REGISTRATION NUMBER: 31,287 REFERENCE/DOCKET NUMBER: HOE 92/F 384 IELECOMBUNICATION INFORMATION: TELEPHONE: (908) 231-4079
                                                                                                                                                                      COMPUTER: IBM 386
OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DAITA:
APPLICATION NUMBER: US/09/160,376A
FILING DAIE: December 1, 1993
CLASS/FICATION GATA:
APPLICATION MATA:
APPLICATION MOMBER: GE P 4240420.7
FILING DAIE: DECEMBER 2, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,060B
FILING DATE: G8-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALILIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE CHARACTERISTICS:
LENGIH: 63 Amino Acids
TYPE: Amino Acid (AA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 52; Conservative
                                                                     New Jorsey
C.S.A.
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                      STREET: Rt. 201 CITY: Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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20005-3315
                                                                                                            08876-1258
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                                             CITY: SON
STATE: NE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 08-291-060B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
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1 FUNCHICOSHIUPEALYINGSERGFFYFPKTRGIVEGGGGGGGGGGGGGENTGN 53
                        Ouery Match 106.0%; Score 254; DR 1: Length 56; Best Local Similarity 100.0%; Pred: No. 4.56-29; Matches 52; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                             APPLICANT: Obermeler, Rainer
APPLICANT: Obermeler, Rainer
APPLICANT: Judwig, Jurgen
APPLICANT: Judwig, Jurgen
APPLICANT: Sabel, Walter
TITLE OF INVENTION: Process for Obtaining Instiln Having
TITLE OF INVENTION: Correctly Linked Cystine Bridges
NUMBER OF SEQUENCES: 12
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Process For Obtaining Profession TITLE OF INVENTION: Possessing Correctly Linked TITLE OF INVENTION: Cystine Bridges
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1800 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARCOLL'N Release #1.0, Version #1.25
CURRUT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: Elbaudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 02481.1424-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEPHONE: 202-408-4000

INFORMATION FOR SECIID NO: 11:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C. United States of America
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                                                                                                                                                    : Sequence 11, Application US/38389487
; Patent No. 5663291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORMATION:
APPLICANT: Chermolet, Ratter
APPLICANT: GGEL, Martin
APPLICANT: Ludwig, Jurgen
APPLICANT: Sabol, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 amine acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide US-08-389-487-11
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CLASSIFICATION: 530
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                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Oberme
APPLICANT: Gerl, I
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US-08-160-376A-6
                                                                                                            RESULT 2
US-08-389-487-11
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Farent No. 5728543
FAREAL THORMATION:
APPLICANT: Molier, Klaus-Peter
APPLICANT: Marquardt, Religer
APPLICANT: Marquardt, Marq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P. STREET: 1800 I Street, N.W.
COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STCRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ALDRESS:
ADDRESSEE: No. 57504970 No. 57504970 No. 57504971h America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEOCCTSICSLYQLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuery Match 100.0%; Score 294; DB 1; Length 96; Best Local Similarity 100.0%; Pred. No. 8.8e-29; Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  APPLICANT: Dudig, Jurgen
APPLICANT: Sabel, Walter
TITLE OF INVENTION: Process for Obtaining Insulin Having
TITLE OF INVENTION: Correctly Linked Cystine Bridges
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett, ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Massington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Taw PC compatible
COMPUTER: Taw PC compatible
COFERATING SYSTEM: PC-DCS/MS-DCS
SOFFWARD: Pationtin Belease #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/389.487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Binaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/CKET NOMBER: 02481.1424-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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Patent No. 5756497
GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Hatstrom, John
APPLICANT: Maistrom, John
APPLICANT: Maistrom, Asser Sloth
APPLICANT: Markussen, Jan
                                                                                                                                  Sequence 8, Application US/08389487
Patent No. 5563291
                                                                                                                                                                                                    APPLICANT: Obermeler, Rainer APPLICANT: Gerl, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                 GENERAL INFORMATION:
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US-08-389-487-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM IYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 2
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US-08-400-256-39
                                                                                                             US-08-389-487-8
                                                                                                                                                            Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 64:
                                                                                                                                                                                                                                                                                                                                         O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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APPLICANT Gerl, Martin
APPLICANT Gerl, Martin
APPLICANT Gerl, Martin
APPLICANT Gerl, Martin
APPLICANT Sabel, Watten
TITLE OF INVENTION: Process for Obtaining Proinsulin
TITLE OF INVENTION: Possessing Correctly Linked
TITLE OF INVENTION: Cystine Bridges
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mcnoeth A. Gandi, Esq.
STREET: Mt. 202-206 No. 5473649th/P.O. Box 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Process for Obtaining Proissulin
Possessing Correctly Linked
Cystine Sridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ċ
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                                                                                                                                                                                                                                                                                             100.0%; Score 294; UB 1; 100.0%; Pred. No. 5.9e-29;
REFERENCE/DOCKET NUMBER: 02481.1105-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                       0; Mishalches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barbara V. Maurer: ESq.
REGISSPRATION NUMBER: 31,287
REFERENCE/POOKET NUMBER: HOE 92/F 384
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/208/160,376A FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/Obi63376A
Patent No. 5473049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WINDOWS 3.1
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                TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4366
TELEFAX: (202) 408-44-00
INFORMATION FOR SEQ 10 NG: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0
Best Local Similarity 100.0
Matches 52: Conservative
                                                                                                                                LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               Similarity 100.
52, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGIH: 96 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino Acid (AA)
                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 08876-1258
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Somerville
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1BM 386
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US-08-160-376A-5
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                                                                                                                                                                                                                                                US-08-291-0608-5
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                                                                                                                                                                                                                                                                                          Query Match
Best Local S1
Matches 52)
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ATTORNEY AGENT INFORMATION:
NAME: Lambiris, Elias 5.
REGISTRATION NUMBER: 33,728
REPERVICE/COCKET NUMBER: 3985,226-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-6123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Halstrom, John
APPLICANT: Jonassen, 1b
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-400-256-45
: Sequence 45. Application US/08400256
: Datent No. 5750497
: GENERAL INFORMATION:
                                                            INFORMATION FOR SEQ ID Not 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Havelund, Svend
Halstrom, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 145 amino acids
                                                                                                                             : 137 amino acids
amino acid
212-867-0123
212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obery Match
Best Local Similarity 100.0
The American S2; Conservative
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Best Local Similarity 100.0
warrhes 52, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :OPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-400-256-45
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                                                                                                                                                             TYPE: am
ICPCLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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: 405 Lexington Avenue, 64th Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 294; DB 1; Length 137; 100.0%; Pred. No. 1.3c-28; Live 0: Mismatches 0; Indels
                                                                                                         ZIF: 10.47-0-00.

COMPUTER FROMMER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Dim Pr Compatible
COMPUTER: Dim Pr Compatible
COMPUTER: Dim Pr Compatible
COMPUTER: Dim Pr Compatible
COMPUTER: District Release #1.0, Version #1.25
CURRENT APPLICATION DARF:
APPLICATION NUMBER: US/06/400.256
FILING DATE: 03-MAR-1995
CLASSIFICATION: DARF:
ATORNEY/ACENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTATION NUMBER: 3985.220-US
TELEROME ZI2-667-0123
TELEROME. 212-67-0123
TELEROME. 212-67-0123
TELEROME. 13-67-0123
TELEROME. 13-67-0124
TELEROME. 
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5)/400.256
FILING DATE: 03.MAR-1995
ATTORNEY/AGENT INFORMATION:
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COUNTRY: United States of America
ZIP: 10174-6491
                                      New York
. United States of America
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jonassen, 1b
APPLICANT: Andersen, Asser Stoth
APPLICANT: Markussen, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-975-365-39; Sequence 39, Application US/08975365; Patent No. 6011007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Havelund, Svend
Halstrom, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 137 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 52, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPCLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                         10174-6401
      New York
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STREET: 40
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APPLICANT:
                                STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPCLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-4C0-256-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 FVNQHIGGSHLVEALYTYCGERGFFYTPKIRGIVEQCCTSICSLYQLENYCN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FVNQELCGSHLVEALYLVCGERGFFYTPKIRGIVEQCCTSICSLYQLENYCN 52
                                                                                  1 FVNQHLCGSHLVEA:/YLVCGERGFFYTPKTRG1VEQCCTSICSLYQLENYCN 52
                                           0;
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Length 137;
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03.9AR-1995
CLASSIFICATION: 514
  100.0%: Score 294; DB 3;
100.0%: Pred. No. 1.3e-28;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 294; US 1; 100.0%; Pred. No. 1.4e-28; ive 0; Mismatches 0;
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us-09-423-100-5.rai

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No. 60110070 No. 6011007disk of No. 6011007tl, America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
SIATE: New York
COUNTRY: JULIA States of America
ZIP: 16174-6401
COMPUTER READARIE FORM:
MEDIUM TYPE: Ficppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 294; DB 1;
Local Similarity 100.0%; Pred. No. 1.4e-28;
Nes 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIREEI: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lambitis, Ellas J.
REGISTRATION NUMBER: 33,728
REFERENCE/LOCKET NUMBER: 3965.220-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-667-0123
TELEPHONE: 212-667-053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Havelund, Svend
APPLICANT: Haistrom, John
APPLICANT: Johassen, Jb
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 38/400,256
FILING DATE: 03:MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48. Application US/08975365
Fatent No. 6011007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEC ID NO: 48:
                                                                                                                                                                                                    03-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 146 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCLECULE TYPE: protein
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                       FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-08-975-365-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
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                                                                                                                                                                                                                                                       TITUE OF INVENTION: ACYLATED INSULIN
NUMBER OF SECUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6011007c No. 6011007cisx of No. 6011007ts America. Inc.
STREET: 465 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5756497disk of Mo. 5756497th America. Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 294: DH 3: Langth 145: 100.0%; Pred. No. 1.46-28; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
ZIP: 10774-6401
ZOMPUTER READABLE FORE
MEDIAN IYPE: Floppy disk
COMPUTER: TAM PC compat.ble
OPERATING SYSTEM: PC-POSS/MS-DCS
SOPWMARE: Patenti Release #1.0. Vorsion #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 57554970 No. 70000 STREET: 405 Lexington Avenue, 54th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Havelund, sven1
APPLICANT: Hals.rom, John
APPLICANT: Johnston, John
APPLICANT: Johnston, John
APPLICANT: Markusson, Jan
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3985.220-03
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10174-6401
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: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NIMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/975,365
FILING DATE:
CLASSIFICATION: 53,4
PRIOR AFFLICATION DATA:
                                                                                                                                                                      APPLICANT: Johassen, 15
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/03400256
Patent No. 5750497
          Sequence 45, Application US/08975365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.728
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TELEPHONE: 212-657-0123
TELEFAX: 212-678-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lambir's, Elias J. REGISTRATION NUMBER: 33.7 REFERENCE/DOCKET NUMBER:
                                                                                                         Havelund, Svend
Halstrom, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i: 145 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEFAX: 212-678-9655
INFORMATION FOR SEC ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 52; Conserv
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                                        Patent No. 6011007
GENERAL INFORMATION:
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                                                                                                                                          APPLICANT:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFPLICANT: Deil, Peter
APPLICANT: Geisen, Karl
TITLE OF INVENTON: Amorphous Monospherical Forms of Insulin
TITLE OF INVENTION: Derivatives
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 53;
                                                                                                                                                                                                                                                                                  99.0%; Score 291; DB 1; Length 57; 98.1%; Pred, No. 1.2e-28; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.4%; Score 283.5; DB 1; Length 98.1%; Pred. No. 8.8e-28;
Live C: Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPALIALE
COMPUTER: IBM PC 505/MS-DOS
SOFTWARE: Patentl: Release #1.0, Version #1.25
SOFTWARE: Patentl: Release #1.0, Version #1.25
SOFTWARE: Date: 25.000 DATE: 25.000 PFLING DATE: 25.000 
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APPLICATION NUMBER: P 43 13 762.4
PILICATION NUMBER: P 43 13 762.4
FILICATION NUMBER: P 193
ATIONEY/AGENT INPORMATION:
NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,220
REPENDE/POOKET NUMBER: 02481.1374-0306C
TELEPHONE: 202.406.4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dunner
SIREET: 1300 I Street, N.W., Suite 700
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CS-08-235-617-4
Fordence 4, Application US/08233617
Patent No. 546666
CENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                   . 7 5
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Sabel, Walter
Deil, Peter
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TYPE: amino acid
TOPOLOGY: linear
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Matches 52, Conservative
                          INPORMATION FOR SEQ ID NO:
SECUENCE CHARACTERISTICS:
LENGTH: 57 aming actids
                                                                                           : 57 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                       MOLECULE TYPE: peptide US-08-030-731A-44
                                                                                                                                                                unknown
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CITY: Washington
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Best Local Similarity
Matches 51; Conserv
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ZIP: 20005-3315
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                                                                                                                                                         TOPOLOGY:
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STATE:
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                                                                                                                                                                                                                                                                               Sequence 44, Application US/CF030731A
Patent No. 5426036
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Riess, Guenther Johannes
APPLICANT: Wilmen, Eugen
APPLICANT: Wilmen, Eugen
APPLICANT: Wilmen, Eugen
TITLE OF INVENTION: Processes for the Preparation of Foreign
TITLE OF INVENTION: Proteins in Streptomyretes
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                      Obery Match
Best Local Similarity 100.0%; Pred. No. 1.44-28;
Matches 52: Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM FOR Compatible

OPPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/06/036,731A

FILING DATE: 12-MAR-1993

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Garrett.
ADDRESSEE: Dunner
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REGISTRATION NUMBER: 34,351
REPRENCE/COCKET NUMBER: 02481-0593-02000
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 155 07/735,757
FILING DATE: 29-20L-1991
PRICH APPLICATION DATA:
APPLICATION NUMBER: DE P 37 :4 866.4
FILING DATE: 05-MAY-1987
PRICH APPLICATION DATA:
APPLICATION NUMBER: DE P 37 :37.8
FILING DATE: 05-MAY-1987
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1300 T Street, N.W., Suite 700
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APPLICATION NUMBER: JS 07/188,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: (IS 67/687,610 FILING DATE: 19-APR 1991 PRICK APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 677410,622 FILING DATE: 01-NOV-1969 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE P 40 12
PILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATE: 03-NOV-190U
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
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                MOLECULE TYPE: protein US-08-975-355-48
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PB : FUNCHICGSHIPPALTIPCSENGFFTIPKTRRGIPGGCCTSICSLYGLENTCH 55

RESHLT: 15

US-08-981-9884-42

US-08-981-9884-42

SEQUENCE 15

SEQUENCE 4.2 APPLICATION: US/1998:988A

PAPELICANT: Vittal MAILY Scientific Research Foundation: APPLICANT: Vittal MAILY SCIENTIFIC RESEARCH FOUNDATION: APPLICANT: THOR OF INVENTION: Insulin NUMBER OF SECURESCONDENCES: 4

CORRESCONDENCES: 4

CORRESCONDENCES: 4

CORRESCONDENCES: 4

COMPUTER REACHAGE

FILING DATE: COMPUTER SCIENTIFIC STREET

COMPUTER REACHAGE

COMPUTER REACHAGE

FILING DATE: SCIENTIFICATION NAME: US/06/381,968A

FILING DATE: COMPUTER STICS:

LEAGUE AND ACTER STICS:

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Qy Ch Search completed: September 15, 2003, 12:05:32 Job time : 11.9284 secs

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September 15, 2003, 12:03:35 ; Search time 21:8065 Seconds (without alignments) 347.945 Million cell updates/sec
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/con2_6/ptodata/1/pubpaa/USG3C_FUBCOMB.pep.*
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/cqn2_6/ptcdata/1/pubpaa/US06_NFW_PUR.pep.*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuden 11d.
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Maximum Match 100*
Listing first 45 summaries
                                                                                                                                                                                                                                  using sw model
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Gapop 16.0 / Gapext 6.5
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Maximum DB seq length: 200000000
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294
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12:
13:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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294 100.0 52 14 US-10 054-873-5 Sequence 5. 294 100.0 150 14 US-10 054-873-5 Sequence 6. 294 100.0 150 14 US-10 054-873-5 Sequence 6. 278.5 94.7 51 14 US-10 054-873-5 Sequence 7. 278.5 93.7 124 10 US-10-98 894-771-18 Sequence 7. 275.5 93.7 124 10 US-09-864-771-19 Sequence 7. 275.5 93.7 124 10 US-09-864-771-19 Sequence 15. 257 90.8 86 16 US-09-864-861-871-19 Sequence 17. 267 90.8 86 11 US-10-058-810-2 Sequence 7. 267 90.8 86 14 US-10-058-810-2 Sequence 7. 267 90.8 96 10 US-09-947-563-4 Sequence 7. 267 90.8 10 US-09-947-563-4 Sequence 7. 267 90.8 10 US-09-15-229-5 Sequence 7. 267 90.8 10 US-09-15-229-5 Sequence 7. 267 90.8 10 US-09-15-229-5 Sequence 7. 267 90.8 110 US-09-815-229-5		Score	Suery	Length	ж К	Q.	Descr:ption
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278.5 94.7 51 11 US-09-658-9358-5 Sequence 5. 278.5 94.7 51 14 US-09-658-9358-5 Sequence 5. 275.5 93.7 124 10 US-09-658-9358-5 Sequence 7. 275.5 93.7 124 10 US-09-661-687-19 Sequence 18. 273 92.9 50 14 US-10-066-009A-3 Sequence 19. 267 90.8 86 10 US-09-678-580-1 Sequence 19. 267 90.8 86 14 US-10-028-411-2 Sequence 4. 267 90.8 86 14 US-10-024-411-2 Sequence 4. 267 90.8 86 14 US-10-054-873-4 Sequence 4. 267 90.8 10 US-09-265-683-12 Sequence 7. 267 90.8 110 US-09-265-683-12 Sequence 7. 267 90.8	٣	294	100.0	150	14	US-10-054-873-7	r.
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267 90.8 86 16 US-69-878-180-1 Sequence 1, 267 90.8 86 14 US-10-028-410-2 Sequence 2, 267 90.8 86 14 US-10-028-410-2 Sequence 3, 267 90.8 86 14 US-10-054-873-4 Sequence 4, 267 90.8 96 10 US-99-947-563-4 Sequence 1, 267 90.8 10 US-09-165-563-12 Sequence 1, 267 90.8 10 US-09-165-229-5 Sequence 1,	œ	273	92.9	50	7	US-10-066-009A-3	
267 90.8 86 11 05-09-858-9358-4 Sequence 4, 267 90.8 86 14 05-10-054-873-4 Sequence 4, 267 90.8 86 14 05-10-054-873-4 Sequence 4, 267 90.8 96 10 05-055-873-4 Sequence 1, 267 90.8 10 0 08-205-858-25 Sequence 1, 267 90.8 10 0 08-205-858-25 Sequence 1, 267 90.8 110 0 08-205-858-25 Sequence 1, 367 90.8 110 0 08-205-858-25	6	267	8.05	86	<u></u>	US-09-878-380-1	
90.8 86 14 US-10-028-416-2 Sequence 2, 90.8 86 14 US-10-054-873-4 Sequence 4, 90.8 96 10 US-047-563-4 Sequence 1, 90.8 110 0 US-09-265-658-126 Sequence 1, 5, 90.8 110 0 US-09-815-229-5 Sequence 3, 5, 90.8	10	267	8.06	86		CS-09-858-9358-4	**
90.8 86 14 US-10-054-873-4 Segmento 4, 90.8 96 10 US-09-947-563-4 Segmento 1, 90.8 110 US-09-265-658-125 Segmento 1.75 90.8 110 C US-09-815-229-3 Segmento 7.75	1	267	8.06	386	7.4	US-10-028-410-2	: N
90.8 96 10 US-09-947-563-4 Sequence 1, 90.8 110 0 US-09-265-658-125 Sequence 1.55, 90.8 110 0 US-09-915-229-5 Sequence 3.7	12	267	8.06	86	-	US-10-054-873-4	-,-
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	15	267	8.08	1.10	۰	US-09-815-229-3	-`.

Sequence 5, Appli Sequence 6, Appli Sequence 1, Appli Sequence 2, Appli Sequence 63, Appli	9 0	10,	. 60.7	6 5, 132, 133,	135, 134, 136, 137,	Sequence 115, App Sequence 14, Appl Sequence 6, Appl Sequence 10, Appl Sequence 805, App
US-09-804-4C9A-9 US-09-969-748C-6 US-10-038-686-: US-1C-328-813-2 US-05-280-030-63	US-09-280-030-62 US-09-736-611-12 US-09-740-359-12 US-09-894-711-12	736-611-10 740-359-10 -894-711-1 736-611-8	10-359- 36-611- 10-359-	894-711 894-711 894-711 65-558-	-205-65 -205-65 -205-65 -205-65	US-09-205-658-115 US-09-815-229-14 US-09-947-563-6 US-09-815-229-10 US-09-925-297-805
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ALIGNMENTS

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RESULT:

10.-10.4-873-5

Sequence 5, Application US/10054873

Publication No. USCOUZOL64712A1

Sequence 1 NFORMATION: Chimeric Protein Containing an Intramolecular Chapterone-Like Sequence Strate: Townsend and Townsenderone-Like Sequence Chapterone-Like Sequence Chapterone-Like Sequence Chapterone-Like Sequence Chapterone-Like Sequence Chapterone-Like Indonesia Indon
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94.78;
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Bost Local Similarity 100.09
warches 52: Conservative
                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: iinear
                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Homo sapiens
09-858-9358-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                        1 PVNQHLCGSHLVBALYLYCGBRGFFYTPKTRGIVEGOTTS:CSLYGLENYCK 52
                                                                                                                                                                                                                             1 FVNQHLGGSHLVBALYIAGGERGFFYTFKTRGIVEGGTSTGSLYGLENYGN 82
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                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application CS/10/54873
Publication No. US20020/64712/1
GENERAL INFORMATION:
APPLICANT: Gen. Zhong Bu
TITLE OF INVENTION: Chimeric Protein Containing an
                                                                                                                                                                    :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.3%; Score 294; UR 14; Lenath 1/7; 100.3%; Pred, No. 5.5e-29; Cive 0; Mismatches 0; indels 0
                                                                                                                           Length 5.25
                                                                                                                                                                 s;apa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentir Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jsn-2002
CLASSIPICATION: <CRNDWAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crow Lip
SIRET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mycroft, Frack J
REGISTPATION NUMBER: 46.946
REFERENCE/DOCKET NUMBER: 020167-000130US
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACIERISTICS:
                                                                                                                       Query Match 105.0%; Score 294; PB 11; Best Local Similarity 106.0%; Pred. No. 2.56-27; Matches 52; Conservative 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/CN96/00052
PTILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 06/423.100
FILING DATE: 11-DEC:2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                               MCLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-873-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: REQ 1D NO: 6: 0S-10-054-873-6
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10054873; Publication No. US20020164712A; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
STRANDEDNESS: «Coknown»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
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Bost Local Similarity 100..
Thes 52: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                       TOPCLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
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Gaps
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APPLICANT: Gall, Zhoug Ku
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dubaquie, Yves
APPLICANT: Dubaquie, Yves
APPLICANT: Lowann, HCHCY B.
TITLE OF INVENTION: METHOD FOR IREATING CARTILAGE DISCRIBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                 COMPUTER READALE FORM:
MADDING ATTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: JBM PC compatible
OPERATION: SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patchin Release #1.0, Version #1.30
                                                                                                                  CORRESPONDENCH ADDRESS:
ADDRESSER: Fownsend and Townsend and Crew LLP
STREET: 140 Embarcaderc Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Myczoft, Frank J
REGISTRATION NUMBER: 45,946
REFERENCE/DOCKET NUMBER: 020167-000130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 294; DB 14;
100.0%; Pred. No. 7.9e-29;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: UDKNOWN>
PRICK APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: WO PCT/CN98/00052
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REPERNCE: P1794R:
CURRENT APPLICATION NUMBER: US/09/056,935B
CURRENT PILING DATE: 2602-07-02
PRICE APPLICATION NUMBER: US 60/248,985
PRICE FILING DATE: 2000-11-15
PRICE FILING DATE: 2000-16
PRICE FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ 1D NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/098589358 Publication No. US20030069177A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                 CITY: San Francisco
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ADDRESSEE: No. US26620193292Alo No. US20025193292Aldisk of No. US20 STREET: 405 Lexisgton Avenue, 64th Floor CITY: Now York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                             72 FVNQHLCGSHLVEALYLVCGERGFFYTPKAAKGIVEQCCTSICSLYQLENYCN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FVNQHLCGSHLVEALYLVCGFRGFFYTPK-TRGIVEOCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDITAL TYPE: F.cppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 4341.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: INSULIN DERIVATIVES NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10066009A
Publication No. US20020165155A1
GENERAL INFORMATION:
APPLICANT: Schaffer, Michelle
APPLICANT: Ulsch, Mark
APPLICANT: Ulsch, Mark
APPLICANT: Vajdos, Felix
ITILE OF INVENTION: CRYSTALLIZATION OF IGF-1
FILE REFERENCE: P1669R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861.687
FILLING DATE: 21 May-2001
CLASSIFICATION: <unitary control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brandt, Jakob
Kurtzhals, Peter
Hanson, Hertz Per
Kaarsholm, Niels Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 68/932,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AITURNEY AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             RESULT 7
IS-09-861-687-19
Sequence 19, Application US/09801687
Publication No. US20020193292A1
GENERAL INFORMATION.
Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                            Jonassen, Ib
Havelund, Svend
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Markussen, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.78;
94.38;
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.3
Matches 50; Conservative
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US-10-056-009A-3
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APPLICANT: Kjeldsen, Thomas Borglum
APPLICANT: Lidvidsen, Stone
TITLE OF INVENTION:
TITLE OF INVENTION: insulin precursor analogues having improved insulin precursor
TITLE OF INVENTION: yield in yeast
TITLE OF INVENTION: WIMBER: PA 2000 00443
PRIOR FILING DATE: 2000-03-17
PRIOR PRIOR APPLICATION NUMBER: 67/211,081
PRIOR PRIING DATE: 2000-02-10
PRIOR PRIING DATE: 2000-02-10
PRIOR PRIING DATE: 2000-02-10
PRIOR PRIING DATE: 2000-02-10
PRIOR PRIING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 20
SOSTWARE: FastSEC for Windows Version 4.0
       Saps
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                                                                       * FVNQHLCGSHLVBALYLVCGERGFFYIPKTRGIVEQCCTSLCSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVILLE HILLS THE FILLS THE FILL STILL SHIP THE FILL SHIP STREET FOR ST. FVINGERGFFYTPKT-GIVESCOTSLOSINGSCHIVON ST.
                                                                                                                 1 FVNOHLGGSHLVEALY LVGERGFFYTPKT-GLVEGCTSIGSLYQLENYCK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.74; Score 278.5; Pe 14; Length 51; 98.14; Pred. No. 26-27;
Uve 0; Mismatches 0; Indels 1
   Indeas
   ..
C; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dubaquic, YVES
APPLICANT: Lowman, Henry
TILLE ON INVENTION: PROTEIN VARIANTS
FILE REFERENCE: P1712R1.
CURRENT APPLICATION NUMBER: US/10/026,410
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US/03/477:324
PRIOR FILING DATE: 2000-01:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18. Application US/39894711 Patent No. US2602013714441
                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10028410 Publication No. US20020160955Ai GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Synthetic US-09-894-711-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.18
Matches 51, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.31
Matches 50; Conservative
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-894-711-18
                                                                                                                                                                                                                                                                                              CS-10-628-410-3
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Matches
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TITEE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                            Cuery Match 90.8%; Score 267; JB II; Length 86; Best Local Similarity 50.5%; Pred. No. 9.4e-26; Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.8%; Score 267; DB 14; Length 86; 60.5%; Pred. No. 9.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew Lip
STRET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2. Application US/10028410

Fublication No. US20020160955A1

GENERAL INCORMATION:
APPLICANT: Dubaquie, Yves

APPLICANT: Lowan, Henry

ITLE CF INVENTION: PROFEIN VARIANIS
FILE REFERENCE: P1712R1-1

CURRENT FILING DATE: 2001-12-19

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 6

SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SLOKKGIVEQCCTSICSLYQLENYCN 86
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               FRIOR APPLICATION NUMBER: US 60/204,490
PRIOR FILING DATE: 2600-05-16
NUMBER OF SEQ ID NOS: 153
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10054873 Publication No. US20020164712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                   OKCANISM: Homo sapiens
US-09-858-9358-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KESUST 11
US-10-028-416-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CS-10-028-410-2
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                                                                                                                               SEQ ID NO 4
                                                                                                                                                                                                    TYPE: PKI
                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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APPLICANT: FUJIREDIO INC.
APPLICANT: FUJIREDIO INC.
APPLICANT: FUJIREDIO INC.
APPLICANT: NURANO, YOSBIDINC
APPLICANT: NAKATSUBO, Kaoru
APPLICANT: NAKATSUBO, Kaoru
APPLICANT: NAKATSUBO, Kaoru
APPLICANT: NAKATSUBO, Kaoru
APPLICANT: NAKATSUBO, Navo
TITLE OF INVENTION: Immunoassay For Measuring Human C-Peptide and Kit Therefor
FILE REPRENCE: 076-022;P
CURRENT APPLICATION NUMBER: US/09/878, 380
CURRENT APPLICATION NUMBER: US 2001-06-12
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-12
NUMBER: PRECEDENCE: NUMBER: SEQ 1D NOS: 2
SOFTWARE: PALENT NOS: 2
SOFTWARE: PALENT NOS: 2
SOFTWARE: PALENT NOS: 2
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Publication No. 082003606917741
GENERAL INFORMATION:
APPLICANT: LOWDAGUIS, YVES
APPLICANT: LOWDAGUIS, YVES
APPLICANT: LOWDAGUIS, YVES
FILE REFERENCE: P179431
CURRENT APPLICANTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REFERENCE: P179431
CURRENT FILING DATE: 2000-01-02
PRIOR APPLICATION NUMBER: US 50/248,985
PRIOR FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 273; DB 14; Lough 50;
Prod. No. 9.56+27;
0; Mismatches 0; lodels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.8%: Soure 267; DR 10; Londth 80;
Best Local Similarity 60.5%; Pred. No. 9.40-26;
Matches 52; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FVNGHLOGSHLVEALYLVCGERGFFYTPKT - - - · ·
CURRENT APPLICATION NUMBER: US/13/066.309A CURRENT FILING DATE: 2002.06.24 PRIOR APPLICATION NUMBER: US 69/287.072 PRIOR FILING DATE: 2001.04.27 PRIOR APPLICATION NUMBER: US 60/267.977 PRIOR FILING DATE: 2001.02-09 SEQ 10 NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 FELLIFOLDEL ELLE ... SECONDE EL SEQUENÇON BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09878390
Patent No. US20020160435A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.2%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Womb sapiens US-09-878-380-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-09-858-9358-4
                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-065-009A:3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
AFPLICANT: Ogc, SCOTE
ITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
ITLE OF INVENTION: IMPAIRED GLUCOSE FOLERANCE CONSTITUENS
FILE REFERENCE: 00786/351004
                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
O
                                                                                                                                                                                                                                                                                                                                                                                              90.8%; Score 267; DB 10;
60.5%; Pred. No. 1.1e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.8%; Score 267; DB 9; Best Local Similarity 60.5%; Pred. No. 1.2e-25; Matches 52; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRENT FILING DATE: 1998-12-03
GORRENT FILING DATE: 1998-12-03
GARLIER RAPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1997-05-05
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEC ID NOS: 328
SOFTWARE: PASLESQ for Windows Version 4.0
SACIO ID NO 125
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : FVNOHLCGSHLVEALYLVCGERGFFYTPKI
                                                                                                                                                                                                                                                                                                              LOCATION: 1..96
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 ----RGIVEQCCTSICSLYQLENYCN 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 SLOKRGIVEÇÜCTSICSLYQLENYON 96
                  IELEPHONE: (202) 408-4400
IELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 125, Application US/09205658
Patent No. US20010029617A:
  FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Sequence 3, Application US/09815229
                                                                                                              LENGTH: 96 amino acids
                                                                                                                                                                                                                                            ORGANISM: Escherichia
                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                     TOPOLOGY: linear
NOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.59
Matches 52, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Homo sapiens
US-09-205-658-125
                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-205-658-125
                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESCLT 15
US-09-815-229-3
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ADDRESSEE: Fincegan, Henderson, Farrabow, Garrett s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.8%; Score 267: DB 14: Length 95:
60.5%; Pred. No. 9.4e+26;
tive 0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-LOS
SOFTWARE: Patentin Release 41.6, Version #1.30
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/09/947,563
FILING DATE: 07-Sep-2001
CLASSIFICATION: <URKNOWN>
             OPERATING SYSTEM: PG-DOS/MS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/10/054,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Umproved process for obtaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDouell
REGISTRATION NUMBER: 33,872
REFERENCE/JOCKET NUMBER: 02481.1666-99690
                                                                                                                                                                                                                                                                                     NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/COCKET NUMBER: 020167-00013605
                                                                                                       FTLING DATE: 22-Jan-2002
CLASSIFICATION: crnknown>
PRIOR PRELICATION DATE:
APPLICATION NUMBER: WO PCT/CN98/D0052
FILING DATE: 31-M/R-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2003
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TOPQLOGY: Linear NOLECTIA TYPE: protein SEQUENCE DESCRIPTION: NEW TO NO: 4: US-10-054-873-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA
APPLICATION NUMBER: 05/134.836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SLOKKGIVEQCCISICSLYQUENYON 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ----RGIVEQCCTSICSLYOLENYCN 52
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rubroder, Franz-Josef
Keiler, Reinhold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300 I Street, N.W. CITY: Washington STAIE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application GS/0947563
Patent No. US20320156234Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.55
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEC 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-947-563-4
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Search completed: September 15, 2003, 12:23:36 • Job time: 22,8065 secs

11:111111111111 TITLI 11111 TITLI 1
25. FVNQHLGGSHLVBALYLVGGRGGFFYTPKTRRBAEDLQVQQVELGGGFGAGSTQFGATEG 84

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GenCore version 5.1.6
Copyright (c. 1993 - 2003 Compugen 1.cd
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	[e]	September 15, 2003, 11:56:45 ; Search time 8.57348 Seconds
	om ws pais	8003, 11:5
(2) 2::5t + (4) 2	OM protein - protein search, using sw model	Soptember 15, 3
	OM protein	Run on:

(Without alignments) 583.284 Mallion cell updates/sec TO NUMBER OF STREET STREET US-09-423-130-5 Perfect score:

PVNQHLCGSHLVEALYLVCG. BLOSUM62 Gapop 10.0 , Gapext 6.5 Scoring table: Sequence:

283308 seqs. 96168582 residues Searched:

283358 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000060000

Post-processing: Minimum Match 190% Maximum Match 190% Listing first 45 summaries

PIR_76:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result heing printhely and is derived by analysts of the total score distribution.

SUMMARIES

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Result		Ouery				
. CN	Score	Match	Length DB	Ē	61	Description
r-1	273.5	93.0	5.1		LIMMIL	ds crees and assign
7	273.5	93.0	51		EHMNI	insalls - finback
m	273.5	93.0	5.1	:	150 N. H	::
च	273	92.9	96	~;	PC7082	- curs
Ľ١	271.5	92.3	51	i	INHY	
9	268.5	91.3		. :	TNMSSP	insulin - Edyptian
7	267.5	91.0	51	: :	A59151	1
80	267	90.8			: PHC	
6	267	90.8	011	C4	B42179	.:
10	267	90.8	011	r.	A42179	52
11	267	90.8	110	r:	200178	=
12	263.5	9.68		. :	INWH1S	C
13	263.5	9.68		. 1	TNCT	
14	263.5	9.68	51		AMUMH	insulin - Arabian
15	263	89.5		. :	IPPG	Ċ
16	263	89.5		. :	LAKS	.:
17	262.5	89.3		:	INCT	1 :
18	252	89.1	110	:	IPPG	
19	261.5	68.3	5	:	OSYMNI	C.
20	260	88.4	110	C:	148166	IG :
2.	258.5	o. 68		. :	IPBO	insuling produkti
22	256.5	87.2		::	JQ0362	::
23	252.5	85.9	77	. •	INSH	in pr
24	252	85.7		. :	IPHC	LOSATIONAC DETRETS
25	251.5	85.5		. :	INCB	
26	251	85.4	1	e:	A39883	10.00
27	250	85.0			INMS1	ے. د
28	249	84.7	110	. :	IPRT1	insulin 1 promise
59	248.5	84.5	51	. •	INGS	- 9:

RESULT 2

NAHE

insulin - finback whale (tentative sequence)
Cispectes: Balaenoptera physalus (finback whale, common rorqual)
Cispectes: Balaenoptera physalus (finback whale, common rorqual)
Cispectes: 11.Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Cispectes: 31.Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Cispectes: 56, 265-293, 1964
A.Title: The amino acid sequence in fin-whale insulin.
A.Reference number: A91916
A.Accession: A91916
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
Cisperfamily insulin
Cisperfamily insulin chain B #status experimental <BCH>

~1	insulin 2 precurso	н	insulin I2 - North	insulin - crested			insulin - black-be		insulin precursor	insulin - Amphiuma	insulin - duckbill	insulin precursor			insulin - alligato
IPRT2	INMS2	S44469	S44470	Odni	INTK	LNOS	A61129	A60414	151221	S61361	863590	IPCH	IPDK	INAQ	INGXA
-	-	7	7	-	~	-	-	(7	7	~	7	-	-	_	_
110	110	52	52	.75	 	in in	27.	.7	103	25	51	107	81	51	52
84.4	94.4	83.7	83.7	83.2	83.2	83.2	83.2	83.2	81.1	81.0	80.1	79.8	79.4	78.7	78.6
248	248	246	246	244.5	244.5	244.5	244.5	244.5	238.5	238	235.5	234.5	233.5	231.5	231
∵	31	32	33	*	35	9	37	æ æ	on on	c)	-,,	7.5	e. *3	7.5	5.5

ALIGNMENTS

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Observiors: Physician catodon (sperm whale)
Clude: 31 Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Clude: 31 Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Clude: 32 Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Clude: 32 Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
Mature 18: 1468-1469; 1558
Mature 18: 1468-1469; 1558
Maritale: Structure of Sperm and Sei-whale insulins and their breakdown by whale parterence number: A93142
Architector number: A93142
Architector in 196: 1-51 A17-428, 1956
Architector number: A90082
Allite: Species differences in Insulin.
Allite: Species differences in Insulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superjacily: insulin

C:Keywords: hormone: pancreas

F:1-30/locals: insulin chain B #status experimental <BCH>

F:1-30/31-51/Product: insulin #status experimental <MAI>

F:31-51/Docals: insulin chain A #status experimental <ACH>

F:31-51/Docals: insulin chain A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 93.0%; Score 273.5; DB 1; Sest Local Similarity 96.2%; Pred. No. 1.5e-24; Matches 50; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Accession: A90082
A.Molecule type: protein
A.Residues: 1-30;31-51 <HARS
                                                             insullo - sperm whale
RESULT 1
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C:Accession: A01591
R:Buenzli, H.F.; Humbel, R.E.
R:Buenzli, H.F.; Humbel, R.E.
A:Dipc:Sayler's L. Physiol. Chem. 353, 444-450, 1972
A:Title: Isolation and partial structural analysis of insulin from mouse (Mus musc A):Reference number: A01591; MUID:72189454; PMID:5028210
A:Contents: composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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Protein Pept. Lett. 6, 15-21, 1959
Agritle: Jack bean seed coat contains a protein with complete sequence homology to
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NiAlternate names: hypoglycemic agent; plant insulin
Cispecies: Canavalia cusiformis (jack bean)
Cibate: 07-Dec-1999 *sequence_revision 07-bec-1999 *text_change 10-Dec-1999
CiAccession: B59151: A59151
                                                                                                                                                               C.Species: CriceLinae gen. sp. (hamster)
C.Cate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C.Ancession: A91456
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C:Species: Acomys cahirinus (Egyptian spiny mouse)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wincelon, F.A.; Delcher, H.K.; Steinman, H.; Lebevitz, H.B.
Fed. Froc. 32, 300, 1973
Ajfilie: Structure of hamster insulin: comparison with a tumor insulin.
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A:Accession: A91456
A:Molecule Type: protein
A:Residies: 1-30:31-51 (NEE)
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A. Title: Species variation in the amino acid sequence of insulin.

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A. Reference number: A90029; MUID:66160119; PRID:5949533

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A. Molecule type: protein

A. Molecule type: protein

A. Residues: 1-30;31-51 <SMT>
A. Note: the species of eleptant is not given, but it is most probably the Indian eleptant

A. Note: the species of eleptant is not given, but it is most probably the Indian eleptant

C. Superfamily: insulin chain B #status experimental -MATT

F. F. B. S. Product: insulin a *status experimental -MATT

F. B. C. Promain: insulin a *status experimental -AACH>

F. B. C. Sportant insulin chain a *status experimental -AACH>

F. B. C. Sportant insulin chain a *status sexperimental -AACH>

F. B. C. Sportant insulin chain a *status sexperimental -AACH>

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C.Date: 24-Apr-1984 *scquencc_revision 30-Sep-1988 *text_change 16-5nl-1999
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F)1-30,31-51/Product: insuin: *status experimental - MAT>
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93.0%; Score 273 5: D# 1

Best Local Similarity 96.2%; Pred. No. 1.5c 24:
Matches 56; Conservative 0: Mismatches 1
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R; Smith, L.F.
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Risieber, P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.
Helv. Chim. Acta 57, 2617-2621, 1974
Arfitle: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindun
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C.Dute: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C.Accession: B42179; A67332; S16494; S22056
R.Seino, S.; Bell, G.I.i, M.H.
Mol. R.Ol. 9, 193-203, 1992
A.Title: Sequences of primate insulin genes support the hypothesis of a slower rat A.Reference number: A42179; MuID:92219953; PMID:1560757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTILLS: The Synthesis of C-peptide of human proinsulin.

A:Reference number: A91658; MUID:73040007; PMID:4803534

A:Concents: annotation; Synthesis of residues 57-87

A:Concents: A: Jaeger, 3: Koenig, W.

Chem. Ber. 106, 2347-2352, 1973

A:Title: Synthesis of the complete sequence of human proinsulin C-peptide and its
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A:Contents: annotation; synthesis of residues 57-87
B:Raufmann, C.E.; Irminger, J.C.; Haiban, P.A.
B:Rochem, J. 310, 869-974, 1995
A:Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide A:Rererence number: S58661; MJID:96013185; PMID:7575420
A:Contents: annotation; site-directed mutagenesis study of proteolytic processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Reference number: A91636, MUID:75077277; PMID:4443293
A:Concents: annotation; synthesis
A:Concents: disulfide-bonded human insulin was synthesized; the synthetic hormone was A:Note: article in German with English abstract
R:Naithani, V.K.
                                                                                                                                                                           A:Molecule type: protein

R:Residues: 57-87 <ROA>

R:Lucasson, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froquel, P.; Lathrop, I.

R:Lucasson, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froquel, P.; Lathrop, I.

Rature Genel, 4, 305-320, 1993

A:Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.; Kb.:

A:Reference number: IS8114; MUID:93364428; PMID:8358446
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A:Residues: 1-59,63-116 <RES>
A:Cross-references: GB:115440; NID:9307071; PIDN:AAA59179.1; PID:9307072
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A:Reference number: A9118b; MUJD:71257722; PMTD:5560404
A:Accession a9118b
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AJMap position: 11p15.5-11p15.5
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Matches 52, Conserv
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The two chains are probably produced from the same preemison
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                       A:Molecule type: protein
A:Residues: 31-51 <MACA>
C:Comment: The two chains are probably prediced from the C:Superfamily: insulin
E:1-30.31-51/Product: insulin Fistatus experimental <MAT>
F:1-30/Domain: chain B *Status experimental <MBAP>
F:31-51/Domain: chain A *Status experimental <CHBAP>
F:31-51/Domain: chain A *Status experimental <CHBAP>
F:7-37,19-50,36-41/Disulfide bonds: *Status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                              91.0%; Score 267.5; DB 2; 92.3%; Pred. No. 7.2e-24;
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A;Residues: 57-87 <0YE>
BOYEN SONTH D.G.: Markussen, J.: Sundby,
Bur. J. Blochem. 20, 190-159, 1571
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Best Local Similarity
Loc 48; Conserva
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C.Species: Balaenoptora borealis (sei whale)
C.Species: Balaenoptora borealis (sei whale)
C.Cato: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C.Cato: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C.Sacossion: A01582
A.Title: Structure of sperm- and sei-whale insulins and their breakdown by whale pe A:Title: Structure of sperm- and sei-whale insulins and their breakdown by whale pe A:Title: Structure of sperm- and sei-whale insulins and their breakdown by whale pe A:Accession: A01582
A:Accession:
                                                                                         Privatesan. W.: Gronoberg, J.: Leinewebor, M.: Wengenmayer, F.: Winnacker, B.L.
Jan. 19, 179-183, 1982
A.Filte: Tro naclearide sequence of cDNA coding for preproinsulin from the primate
A.Reforence number: Jug178, MUID:83080474; PRID:5184252
A.Reforence number: Jug178, MUID:83080474; PRID:5184262
A.Residuce: J.-10 VRPA
A.Residuce: J.-110 VRPA
A.Cross-references: GB.J00336; NID:9342121; PIDN:AAA36849.1; PID:9342122
A.Cross-references: GB.J00336; PID:9342121; PID:9342122
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C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 15-Jul-1999
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PVNQHECGSHLVEALYINGGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
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60.5%; Pred. No. 1.6e-23;
Live 0: Mismatches 0; Indels
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A;Residues: 1-30;31-51 <SMI>
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C:Species: Pan troglodytes (chimpanzee)
C:Species: Pan troglodytes (chimpanzee)
C:Species: Pan troglodytes (chimpanzee)
C:Species: Pan Mar1993 = Requence_revision 18 Nov-1994 #text_change 16-Jul-1393
C:Accession: A42179; S22058
R:Seno, S::Bell, G.I., Li, W.H.
Mol. Biol. Evol. 9, 193-203, 195-204
A) Title: Sequences of primate insulin genes support the hypothesis of a sigwer rate of A) Reference number: A42179; MJD:92219933; PMID:1560757
A) Reference number: A42179; MJD:92219933; PMID:1560757
A) Reference number: A42179
A) Reference: Lill C-SEI>
A) Molecule type: DNA
A) Molecule type: DNA
A) Reference extracted from NCBI backbone (NCBIP:97067)
C:Genetics:
C:Genetics: 63/J
C:Superfamily: insulin
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60.5%; Pred. No. 1.66-28;
tive 0; Mismarches 0; Todols
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C;Species: Macaca fascicularis (prab-cating macaque)
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Best Local Similarity 60.5
Matches 52: Conservative
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Best Local Similarity
Thes 52; Conserve
A;Accession: B42179
A;Molecule type: UNA
A;Residues: [-110 <SEL>
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C.Species: Camelus dremedatius (Arabian camel)
C.Species: Camelus 492762
R.Danho, W.O.
J. Fact Med. Saghdad 14, 16-28, 1972
A.Tille: The isolation and characterization of insulin of camel (Camelus dremence number: A92762
A.Tille: The isolation and characterization of insulin of camel (Camelus dremence number: A92762
A.McCession: A92782
A.McCession: A92782
A.McCession: A92782
A.McCession: A92782
C.Superfamily: Insulin chara a status experimental camelus (Camelus dremental camelus dremental characteristic (A) 13.51/Domain: Insulin chara a status experimental camelus (A) 15.7500main: Insulin chara a status (A) 15.7500main: Insulin chara a s
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C.Species: Sus scrofd domestic pig)
C.Species: Sus scrofd domestic pig)
C.Species: Sus scrofd domestica (domestic pig)
C.Species: Sus scrofd domestica (domestic pig)
C.Accessor: A01583 Asequence_rysision 22 Jun-1941
C.Accessor: A01583 Asequence_rysision and action acid sequence.
R.Chance, R.E.: Eliis, R.M.: Bromer, W.W.
Scafence C.B.: 165-167, 1958
A.Title: Portine protein
A.Reference number: A94240, M910:68286488; PMID:Sus7063
A.Accession: A01583
A.Molecule type: protein
A.Residues: 1-34, 70, 36-34
A.Reference number: A94572
A.Accession: A94572
A.Accession: A94572
A.Accession: A94572
A.Accession: B4 4CH2>
A.Reference number: A90344
A.Reference number: A90344
A.Reference number: A90344
A.Reference number: A90344
A.Residues: 1-36:31-51 cBRO>
R.Snel, L.: Dangaard, U.
Horm. Metab. Res. 20, 476-480, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.6%; Score 263.5; DB 1; Senqt5 51; 90.4%; Pred. No. 2.1e-23; ive 1; Mismatches 3; Indels
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C.Superfamily: insulin
C.Keywords: hormone: pancreas
F1-130/Domain: insulin chain B *status experimental <8CH>
F1-130.31-51/Product. insulin *status experimental <ACH>
F31-51/Domain: insulin chain A *status experimental <ACH>
F7-37,19-50,36-41/Disuilide bonds: *status predicted
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Matches 47; Conservative
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A; Eithe: Proinsulin heterogeneity in pigs.

A;Reterence number: A60835: MUD:89032178; PMID:3181865

A;Recession: A60835: MUD:89032178; PMID:3181865

A;Recession: A60835

A;Recide type: protein

A;Residues: 33-39,40-62 <SNE>

A;Recidues: 33-39,40-62 <SNE>

A;Recidues: accounting peptide variant landing the authors report the characterization of a connecting peptide variant landing the authors report the characterization of a connecting peptide variant landing the authors report the characterization of a connecting peptide variant landing the authors report the characterization of a connecting peptide variant landing the characterization of a connecting period the character
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A.Molecule type: protein
A.Roslecule type: protein
A.Roslundeil, 7:/ Dodson, G.; Hodgkin, D.; Mercola, D.
Adv. Protein Chem. 26, 279-402, 1972
Adv. Protein Chem. 26, 279-402, 1972
A;Title: insulin. the structure in the crystal and its reflection in chemistry and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: insulin
C; Keywords: Cormone; pancreas
F; 1-30/Pomain: insulin chain B #status experimental <BCH>
F; 1-30,64-64/Product: insulin #status experimental <MAT>
F; 34-54/Pomain: connecting peptide #status experimental <CPEP>
F; 64-64/Domain: insulin crain A #status experimental <ACH>
F; 64-64/Domain: insulin crain A #status experimental <ACH>
F; 77,0,19-83,69-74/Disulfide bonds: #status experimental
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A)Contenis: annotation: X-ray crystallography, 1.9 angstroms
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60.7%; Prod. No. 3.6e-23;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compagen Ltd.
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- protein search, using sw model

OM protein

2003, ili54:00 ; Search 'ime 4.84588 Seconds (without allements) 504.633 Million cell updates/sec September 15, Run on:

1 FVNQHICGSHIVEALYLVCG.....IVEQCCTSICSLYQLSNYCN 52 US-09-423-100-5 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127853 segs, 47025705 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 Minimum DB seq Maximum DB seq

Listing first, 45 summaries 100% Post-processing: Minimum Match Maximum Match

SwissProt_#1:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		e			SUMMARIES	
Result No.	core	Cuer	Sength	Ē	a	 E.
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2	273.5	ű.		٠1	INS_ELEMA	
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13	256.5	87		~	INS_DIDMA	-
20	254.5	86		-	INS_SHEEP	
21	252	35		٦	INS_HORSE	F01310 equus cabal
22	251.5	85		-	INS_CHIBR	P01327 chinchilla
23	251	99		_	INS_AOTTR	P10504 actus trivi
24	250	ထ			INSI_MOUSE	P01325 mis miscula
25	243	8		-	INS1_RAT	P01322 rattus norv
56	248.5	84		ч	INS_ANSAN	P07454 anser anser
27	248	84		_	INS2_MOUSE	PS1326 mus musculu
28	248	84		7	INS2_RAT	
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31	244.5	93		_	INS_TRASC	trachemy
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P01332 gallus gal	P01333 anas plat;	P12703 alligator	P09476 lepisoster	P12768 zaocys dhu	P01334 crotalus at	P12706 xenopus la	P12707 xenopus la	P14806 petromyzon		P29335 amia calva	
INS_CHICK	INS_ANAPL	INS_ALLM:	INS_LEPSP	INS_ZAODH	INS_CROAT	INSTANTA	INS2_XENLA	INS_PETMA	INS_PLAFE	INS_AMICA	INS_ONCGC
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2. S.	79.4	78.7	78.6	77.7	77.4	77.0	77.0	75.5	73.5	72.8	71.8
o.	233.5	231.5	233	228.5	227.5	226.5	226.5	222	216	214	211
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ALIGNMENTS

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isblhara Y., Saito T., Ito Y., Fujino M.; *Structure of sperm- and sel-whale insulins and their breakdown by whale pepsin."; *Nature 181:1458-1469(1958).
                                                                                        Halaenopiera physaius (Finback whale) (Common rorqual), and Physeter catodon (Sperm whale) (Physeter macrocophalus). Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria; Cetartiodactyla; Cetacea; Mysticcti; Halaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR: A91918; INWHF.
PIR: A93142; INWHP.
                                                                                                                                                                      SPECIES=B.physalus;
Hamm H., Titani K., Sakaki S., Narita K.;
Hamm H., Titani K., Sakaki S., Narita K.;
"The arino acid sequence in fin-whale insulin.";
"I Sicohem. 56:288-293(1964).
                                      01, Created)
01, Last sequence update)
34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSULIN B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   #SSP; P01317; IAPH.
InterPro: IPR04825; Ins/IGF/relax.
SMATT; SMS0078; IIS; 1.
FROSITE: PS00263; INSCLIN; 1.
insulin family; Hormone; Glucose metabolism.
                    51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN.
INTERCHAIN.
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31
51
37
50
41
5766 MW;
                    STANDARD;
                                                                                                                                                                                                                                                                                                          SPECIES=P.catodon;
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31
7
19
36
51 AA;
                                                                                                                                                                                                                                   SPECIES-P.catodon;
                                     21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
61-OCI-1996 (Rel.
                                                                                                                                                               PARTIAL SEQUENCE.
                    INS_BALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
SECUENCE
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                                                                       insulin.
RESULT 1
INS_BALPH
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9007B514691A7CDD CRC64;

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-:- SUBCELLULAR LOCATION: SCCTCLEG.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
FIR; A01591: INKSEP.
HSSP: P01368: ITXM.
                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
992BD8E629047D3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                         INSULIN B CHAIN.
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                                                                                                                                                                                                                                                                                                                                                          nsulic family; Hormone: Glucose metabolism
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                                                                                                                                                                                                                                                                                                      InterPro: IPR064825: Ins/1GF/relax.
SMAR: SMO6078; I:GF: 1.
PROSITE; PS00262; INSULIN: 1.
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MEDLINE=72258016; Pubmed=4626369;
                                               MEDL:: NE=72189454: PubMed=5028210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcl. Biol. Evol. 9:193-203(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%;
92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                             33.
41
41
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                              NOTIFICATION
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CHAIN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Asseys.
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                                                 Sdpt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
SURBUXI: HETEROIMSR OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULPIDE BONDS.
                                                                                                                                                                                                                                                                                                                          Elephas maximus (indian elephast).
Eukaryota, Metazoa: Chordata; Craniana: Vernekrata: Enteleastomi:
Mammalia: Eutheria: Proboscidea: Elephantidae; Elephas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCREASES CELL PERMEABILITY IC MONOSACCHARTHES, AMINO ACHUS AN
FATIY ACIDS. II ACCELERNTES GLYCOLYSIS, THE PENTOSE PHOSPHATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FVNOHIGGSHIVEALYINGGRRGFFYTPXIRGIVROCTFICSLYQLENYCM 52
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                                                                                                   PONDHIGGERIA HIGHTIGGERIA HIGGERIA GIVENTELLE TELLETTE TIL
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                                                  PVNQHLCGSHLVEALYLVGGERGFFYTPXTRG1VEGCCTS: CSLYGLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBCELLUIAR LOCATION: Secreted
-:- MISCELLUANDOUS: THE SPECIES OF ELFPHANT :S NOT GIVEN, BUT
MOST PROBBLY THE INDIAN ELEPHANT (ELFPHAN MAXIMUS)
-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Species variation in the amine acid sequence of insulin ";
Am. 5. Med. 40:662-666(1966).
-!- FUNCTION: INSULIN DECREASES BLOGD SLUCOSE CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 273.5: DM 7: Length 51:
              Length 51:
            Score 273.5; 38 1; Length 5; Pred, No. 4.9e-27; 0; Mismatches 1; Indels
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es 1;
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21-33L-1986 (Rel. 01, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin family: Hormone: Glicose metabolism.
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NO
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InterPro; IPR004825; Ins/IGE/relax.
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5; PS00262; INSUEIN; 1.
          93.0%;
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     Query Match
Best Local Similarity 96.2*
Matches 50; Conservative
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49; Conservative
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PROSITE;
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Best Local S
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Eukaryota: Metazoa; Chordata: Craniata: Vortebrata; Eutoleostomi;
Mambalia: Eutheria: Primatos: Catarrhini: Cercopithecidae;
Corcepithecinae; Corcepithecus.
                                                                          1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                               51
                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A. MEDDMed-1550757; MEDLINE-92219953; PubMed-1550757; Selio S., Bell G.J., Li M.; Sequences of primate insulin genes support the hypothesis of sicwer rate of molecular evolution in humans and apes than in
                                                                                                 1 FVBQHLCGSHLVEALYLVCGERGFFYTPKS-GIVDQCCTSICSLYQLENYCN
51;
  DB 1; Length
                                    0; Indels
                2e-26;
                                                                                                                                                                                                                            p30407; PC1309;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Sequence update)
01-PEB-1996 (Rel. 33, Last annotation update)
                                      3; Mismatches
  Score 268.5;
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SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE-Pancreas
     Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Froc.
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                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWES lustrate of Bloinformatics and the SMED cutstation. The between Entropy and Entropeas Boinformatics institute. There are no restrictions on its use by non-profit institutions as long as its context is in an way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | HTT | PULL | FILL | F
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SUBCNIT: HETERODINER OF A B CHAIR AND AN A CHAIN CINKED BY TW
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Mammalia, Eutheria, Primanes, Catarrhini, Hominidae, Honco.
NCBL_TaxID=9606;
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MEDLINE-80054779; PubMed-503234;
Bell G.L., Swaln W.F., Pictet R.L., Cordell B., Goodman H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 110;
                                                 SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULIN/IGF/FELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bell G.1., Pictot R.L., Rutter W.J., Cordell B., Tischer
Goodnan B.M.;
"Sequence of the human insulin gene.";
Nature 284:25-32(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12019 MW: 95A1F548E7B247F9 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                #ISSP; P01318; TAID.
InterPro: IPR004025; Ins/16F/relax.
Pfam, PF00049; Institut; 1.
PROSTE; PS00262; INSULIN: 1.
Insulin family; Hormone; Slucose metabolism; Signal.
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Ullrich A., Dull T.J., Gray A., Brosius J., Sur-
"Genetic variation in the human insulin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. Cl. Created)
21-JUL-1986 (Rel. Cl. Last sequence update)
15-SEP-2003 (Rel. 42, Last admonation update)
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INTERCHAIN.
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MEDLINE-80120725; Pubmed-6243748;
                                                                                                                                                                                                                                                                                                                                                  MMBE: X61092; CAA43405.1; -.
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96
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                              SCNOW GCIATOSIC
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Matches 52: Conserv
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P01308:
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MEDLINE=75077277; Pubmed=44443293;
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NCBL_TaxID=9541;
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Best Local Similarity
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                                                                                                                  SYNTHESIS OF 65-69 AND 70-73.
MEDLINE-73161263; PubMed-4698558;
              MEDLINE=75046007; PubMed=4803504;
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SYNTHESIS OF 57-87
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                    His C. X., Weiss M.A.; "Toward the solution structure of human insulin: sequential 2D IN NMK assignment of a des-pentapoptide analogue and comparison with crystal structure.";
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-:- SURGNIT: HEPREDDIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
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Eukaryota; Metazoa: Chordata; Craniata; Vertobrata: Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae:
covel point mutacton in the human insulin gene giving rise to
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-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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Winnacker E.-L.;
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60.5%; Pred. No. 6.3e-26;
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21-400,1986 (Rel. 01, Created)
13-A0G-1987 (Rel. 05, Last sequence update)
13-FBB-1996 (Rel. 33, Last sequence update)
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MEDLINE-83080474; Pubmed-6184262;
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MEDLINE-91242467: PubMed-2036420;
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MEDLINE-91265527; Pubmed-1646635;
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MEDLINE-91104966; Pubmed-2271664;
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Seno 19:179-183(1982)
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the Buropean Bioinformatics institute. There are no costrictions on its muse by comprosit institutions as long as its content. Is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isp sib.ct/ancounce/or send an email to license@lsb-sib.cb).
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Eukaryota: Motaxoa: Chordota; Cruniani: Verrebrata: Surele-scomu;
Kammalia: Eytheria; Primates; Catarrhini; Hominidae: Fan.
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Seino S., Bell G.f., Li M.;
'Sequence of primate insulin genes support the hypothesis of
slower rate of molecular evolution in humans and apps than in
                                                                                                                                                                                                                                                          Length 110:
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SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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SIGNAL 1 24
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Pred, No. 6,30-26;
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01-APR-1993 (Rel. 25, Last Sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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PIR: LQ02178; J00278.
HSSP: P01308: 1A10.
InterPro; IRM04835; Ins/Ins/relax.
Pfam: PFC0049: Insulin; I
PRINTS: PRC0027; INSULNB.
SMART: SM60078; ILGF: I
PROSITE; PS00262; INSCLIN; I.
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-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishihara Y., Saito T., Ito Y., Fujiro M.;
Kiructure of sperm- and sel-whale insulins and their breakdown by
the a nears of sperm-
                                                                                                                                                                                                             Insulin family; Hormone: Clucose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palaenoptera borealis (Sei whale).
Eukaryota, Mctazoa: Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Ealaenopteridae; Balaenoptera.
NORI_TaxID=3768;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 110;
                                                                                                                                                                                                                                                                                                                                                                                            Score 267; DB 1; Length ... bred. No. 6.36-26; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
PIR; A01582; INWELS.
HSSP; RO1317, JAPH.
                                                                                                                                                                                                                                                                                                                                                                                   12025 MW; 41EB8DF79837CEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P013.4;
21-JJL-1986 (Rel. 01, Created)
21-JJL-1986 (Rel. 01, Last Sequence update)
91-JCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                       C PEPTIDE.
INSULIN A CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                     INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                           INTERCHAIN.
send an email to licensedish-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 ----RGIVEOCCISICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI;
                                                           P1R; A42179; A42179.
PDB; 1EFE; 29-MAR-0C.
InterPro; IPR004825; Ins/IGF/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004825; Ins/IGF/relax
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PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           90.88;
                                       EMBL: X61089; CAA43403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 181:1468-1469(1958).
                                                                                                                                                                 SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN;
                                                                                                                     Pram; PF00049; Insulin; 1.
PRINTS; PR00277; INSULINB.
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Best Local Similarity 60,59
Matches 52, Conservative
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54
110
100
100
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P01314;
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41
5692 MW;
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90.48;
  Bovidae, Caprinae, Capra.
NCBL_TaxTD=9925;
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37
50
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                                                                                                                                                                                                                                                                                                                                                            Similarity
47; Conserv
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CHAIN
DISULFID
                                                                    "Species"
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Best Local S
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INS_PIG
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   9
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J. Fac. Med. Bagadad 14:16-28(1972).

J. SUBCELS, LT ACCEMENTES BOOMSACCIANIBES, ANTHO ANTIS AND FATTY ACIDS. JT ACCEMENTES GLYCOLYSIS, THE PENTOSE PHOSFHAIR

J. SUBCHILL HETHORINES OF A B CHAIN AND AN A CHAIN LINKED BY TW. DISCULFIDE BOOMS.

J. SUBCELLULAR LOCATION: Socreted.

J. SUBCELLULAR LOCATION: Socreted.

J. SUBCELLULAR LOCATION: Socreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capra hirous (Goat).
Eukaryota, Metazoa, Chorduta, Craniata, Vertebrata, Euleleastomio
Mammalia, Eutheria, Cetartiodactyla, Euminantia, Precra, Rovosbus
                                                                                                                                                                                                                                 Camelus dromedarius (Gromedary) (Arabian camel).
Bukaryotai Merazoai Chordatai Granianai Veriebraiai Bucelensiomii
Mammaliai Butheriai Cetartiodactylai Tylopodai Gamelidae; Gamelus
NCBI_TaxID+9838:
                                                                  1 FVNQHI.CGSHI.VEALYI.VGGERGFFYTPKIRGIVEQUOTISIOSIIYOJENYON 52
                                                                                                                                                                                                                                                                                                    Dacho W(0)_{\rm c} . The isolation and characterization of tamelus "The isolation and characterization of tamelus
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                      oh 89.6%; Score 263.5; DB 1; Length 51; 1 Similarity 92.3%; Pred, No. 8.2e-26; 48; Conservative C; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.6%; Score 263.5; DB 1; Lenath 52: 90.4%; Pred; No. 8.20-26;
Live 1; Mismatches is Tadels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901E88BA085A7DDD CRC64;
9007BSCE400A7DED CRC64:
                                                                                                                                                                      21-001-1986 (Rel. 01, Created)
21-001-1986 (Rel. 01, Last sequence update)
01-FES-1996 (Rel. 33, Last encotation update)
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21-30L-1986 (Rel. 0), Last sequence update)
61-FER-1996 (Rel. 3), Last aunolation ipdate
                                                                                                                                                  5. AA
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SMART; SM00078; ilGF; 1.
PROSITE: PSGC262; INSULIN; 1.
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5723 NW:
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                                                                                                                                                  STANDARD
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HSSP: P01317; 21NS.
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Matches 47; Conserv
51 AA;
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P01319;
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                      Query Match
Best Local (
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SEQUENCE
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Gaps
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-:- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. 3.T

INCREASES CELL PERMEABILITY TO MONOSACHARIDES, AMINO ACIDS AND
FATTY ACIDS. 3T ACCELERATES GRACOLYSIS, THE PENTOSE PHOSPHATE
CYCLES, AND GLYCOGGEN SYNTHESIS IN LIYVER.

-:- SUBCNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparative sequence analysis of the INS-IGF2-H19 gene cluster in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota, Matazoa, Chordata, Craniata, Vortebrata, Euteleostomi;
Mammalia, Eutheria, Cetartlodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE of 25-108.
MEDLINE-68286485; PubMod:5657063;
Chance R.E., Ellis R.M., Bromer W.W.;
"Portrine profinsulin: characterization and amine acid sequence.";
Science 161:165-167(1968).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FVNQHLGGSHIVEALYIVGGERGFFYTPKA-GIVEQCCAGVCSIXQLENYCN 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 52;
                                                                               variation is the amino acid segmence of insulin. ";
                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLUIAR LOCATION: Secreted.
-i- SIMILARITY: BECONGS TO THE INSULIN/IGE/RELAXIN FAMILY PIR: AC1586; INCT.
BSSP; 101317; IAPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 263.5; DB 1; Lengen.
Pred. No. 8.2e-26; Indels
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"Complete porcine preproinsulin cDNA sequence.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9007B50CDB4E7DDD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN A CHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issuin family, Hormone, Glucose metabolism.
CHAIN 1 30 INSULIN B CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STANIN-Large white,
STATIN-Larges white,
MEDINE-22135958, Pubmed=12140686,
Amerger V., Navyen M., Laere A.S.,
Georges M., Andersson L.)
MEDLINE-66160319/ PubMed-5949593;
Smith L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mamm. Genome 13:388-398(2502).
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                                                                                                                                                                                                                                     MEDLINE-89099318; PubMed-2905485;
Baker E.N., Bundell T.L., Cutfield J.F., Cuttrold S.M., Dodson E.U.,
Dodson G.G., Growfoct Hodykin D.M., Hubbard R.E., Isaans N.W.,
Reynolds C.D., Sakabo K., Sakabo N., Vijayan N.M.,
"The structure of 20m pig insulin crystals at 1.5-A resolution.";
Philos. Trans. R. Soc. Loid., B. Biol., Sci. 319:369-456(1998).
                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
Isaacs N.W., Agarwal R.C.:
"Experience with fast Fourier least squares in the refinement of the crystal structure of rhomoohedral 2-zinc institu at 1.5-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW-"http://www.expasz.ora/spotlight/articles/sptlic0e.html".
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLING-91222450; PubMed-2025410;
Badger J., Harris M.R., Rayboids C.D., Evans A.C., Docson E.L.,
Dodson G.G., Worth A.C.I.
"Structure of the pagins lin dimer in the cipte crystal,",
Acta Crystallogr. B 47:122-136(1991).
                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLAGRAFHY (2.) ANSSTROMS).
MEDLINE-92126280: PubMed-17726/33:
Balschmidt, P., Hansen F.B., Dodson E., Dodson G., Korber F.,
"Structure of porcine insulin cocrystailized will clupcine Z.
Acta Crystallogr. B 47:975-986(1991).
                                                   X-RAY CRYSTALLOGRAPHY (I.) ANGSTROMS).
Bluddell T.L., Dodson G.G., Hodckin D., Mordola D.:
*Insulin, The structure to the drystal and its reflection in
chemistry and blology.";
Adv. Protein Chem. 26:279-402(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. SUBCELULAR LOCATION: Secreted.
-!- SIMILARHTY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
-!- DATABASE: NAME-Protein Spoilight:
-NOTE-ISSUE 9 of April 20011
                  Chance R.B.;
Submitted (301-1970) to the PIR data back.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).
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EMBL; AY044828: AAi:69550.i; -.
PDB; 31NS; 09.CAN-89.
PDB; 41NS; 31-JUL-94.
PDB; 61NS; 31-JAN-94.
                                                                                                                                                                                                   Acta Crystallogr. A 34:782-791(1978).
                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY
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15-OCT-91.
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REVISION TO 59.
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112B;
2TCI;
             Chance R.B.
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25 FVNQHECGSHEVEALYEVCGERGFFYTPKARREAENPQAGAVELGGGIGGTQALAEEGPP 84
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                                                                                                                                                                                                                                                                                                                                           Hormone, Glucose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotá, Metazca, Chordata, Craniata, Vertebrata, Euleleostomi,
Masmalia, Eutheria, Lagemorpha, Leporidae, Oryctolagus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
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Glddings 3.J., Carnegin L.R., Devaskar S.U.;
Submitted (APR-191) to the EMBL/Genbank/DDBJ databases.
-:- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION.
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Menos R.K., Zahm D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species variation in the amino acid sequence of insulin."; Amed. 40:662-666(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 263; DB 1; Length 108; Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11671 MW; CB4491B429858EBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          INSULIN B CHAIN.
C PEPTIDE.
INSULIN A CHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01311;
21-301-1986 (Rcl. 01, Created)
01-FEB-1996 (Rcl. 33, Last sequence update)
01-0CT-1996 (Rcl. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
STRAIN-New Zealand while; TISSUE-Pancroas;
MEDLINE-94179230; PubMed=8132571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 OKKGIVEQCCISICSLYQLENYCN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 -- RGIVEQCCISICSLYQLENYCN 52
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                                                                                                                                                                                                                      InterPro) IPR004825; Ins/1GF/relax. Prfam, PF0049; Insulin; SMAF; SMAF; SMAF; SMAF; 1, PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-66160119; PubMed~5949593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.5%;
60.7%;
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Rest Local Similarity burns
Rest Local Similarity burns
Rest Local Six Conservative
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                                                                                                                                                                                                                                                                                                                                                                            107
29-3AN-96.
29-3AN-96.
16-33N-97.
01-APR-98.
28-FBB-97.
16-FEB-99.
                                                                                                                                                                    28-JAN-98.
28-JAN-98.
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107 1
108 AA;
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                                                                                                                                                                                                                                                                                                                                         Insulin family;
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57
88
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                                                                                     |SDB:
|WAV;
|ZEI;
|ZNI;
|ZNI;
                                3MTH;
                                                          1DEI;
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STRAND
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IPR004825: Ins/IGF/relax
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59,38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A01588; INCT
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CISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               PROPER
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the PMEL offstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its conton. Is no many modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/spcounce/or send an email to license@isb-sib.ch).
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Tredrea M.R., Buck M.J., Guhamiyoqi J., Squirc T.L., Andrews M.T.;
Submitted (JUN-2001) to the EMB/GenBank/DbbJ databases.

-!- FUNCITON: INSULIN BERHAAES BLOOD GLUCCSE CONCENTEATION. IT
INCREASES CELL PERHABILITY TO MONGSACCHARIDES. AKING ACTES AND
FALTY ACIDS. IT ACCELENTES GLYCOLYSIS. THE PENTOSE PHOSPHAIB
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKEL BY TWO
INCREASES CELL PERMEABILITY TO MONOSACCHARITES, AMINO ACIDS AND
                PAITY ACIDS. IT ACCELERATES GLYCOLYSIS. THE PENIOSE PHOSPEATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER. SUBUNIT: HETERODINER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermophilus tridecemlineatus (Thirteen-Lined ground squirrel),
Eukaryota, Metazoa: Cherdana; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Wodestia; Sciurograthi; Sciuridae: Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                          SURCELINIAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULN/IGE/HELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> Y (IN REF. 3).
82D2975B85D77FA8 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                    InterPro: 1P8004825; Ins/;GP/relax.
Pfam: PF66649; Insulin; 1:
MART: SMC079; 1ACF: 1.
PROSITE: PS00262; 1NSUIN; 1.
Insulin family: Hormone: Glucose metabolism: Stinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 263; DB 1;
Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9IXI3;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSULIN B CHAIN.
C PEPTIDE.
INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT: 110 AA
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                                                                                                                                                                                                                                                                                                          EMBL: 003610; AAA19533.1; -. EMBL: M61253 AAA17540.1; -. PIR: A534.8; INPH: HSSP: P01308; INPH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89,58;
59,38;
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                                                                          DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934
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Best Local Simi
Matches 51:
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peiis silvestris catus (Cat).
Eukaryota, Metazou: Chordata; Craniata; Vertebrata; Euteleostomi;
Nammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 110;
DISULFIDE BONDS.
--- SUBCEDULAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 263; DB 1; Lengu. ...
Pred. No. 1.9e-25;
fined. No. has 6; Indels
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-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSULIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
HY SIMILARITY.
4511768D6622HEES CRC64;
                                                                                                                                                                                                                                                                                                                                  HSSP: P01308: 1LNP.
InterPro: IPR046825; Ins/IGP/relax.
Fran: PF00049; Insulin: 1.
PRINTS: PR00277: INSULINB.
PRINTS: PR0078: INSULINB.
PROSTTE: PS00028: INSULINE.
Insulin family: Rormone: Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
INSULIN B CHAIN.
C PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AA.
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Job time
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J. Biol. Chem. 258:2357-2353(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Bukaryota: Metazoa, Chordata; Craniata: Vertebrata: Enteleustomi:
Marmalia; Eutheria; Carnivira: Pissipedia; Canidae: Canis.
                                                                                                                                                                                                                                                                                                                                                                                                            1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                         | HTL-HTHT-HTHT-HTHT-HTHT-T-HTHTL-HTHT-HTHT-HTHT-T-HTHT-HTHT-T-HTHT-T-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTHT-HTH-HTH-HTH-HTH-HTH-HTH-H
                                                                                                                                                                                                                                                                                                 Score 262.5; DB 1; Length 51;
Pred. No. 1.1e-25;
2; Mismatches 2; Indels
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SIMITARITY: RELONGS TO THE INSULTN/TGF/KELAXIN FAMILY.
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Pfam: PF00049; Insulin: 1.
SMART; SM0078: ILGF: 1.
PR0SITE: PS02062; ILGFII: 1.
Insulin family: Hormone; Glucose metabolism; Signal.
SIGNAL 1.
                                                                                                                                                                                                                                                  900735096A0A7DDD CRC64;
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21-J05-1986 (Rel. 01, Last Segmence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                 INSCLIN B CHAIN.
                                                                                                                                       INSULIN A CHAIN.
                                                           Mormone: Glucose metabolism
                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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MEDLINE-66160119: Pubmed-5949593:
                                                                                                        30 31
31 51
19 50
19 50
36 41
51 AA: 5745 WW: 9
SMART; SM00078; IIGF; I.
PROSITE; PS00262; INSULIN; I.
Insulin family; Hormone: Gluc
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90.4%;
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Best Local Similarity 90.4
Matches 47; Conservative
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HSSP; P01317; 1APH.
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CHAIN
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INS_CANFA
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                                                                                                                                    1 FVNQHLCGSHIAVEALYLVCGERGFFYTPKT............
                                                                                                                34; Gaps
                                                                                        Length 110;
                                                                           89.1%; Score 262; DB 1; Length 12:
59.3%; Pred. No. 2.6e-25;
"""marches i; Indels
85 ALOKRGIVEOCCTSICSLYQLENYCN 110
                                                                                                                                                                                 41 ----RGIVEQCCTSICSLYQLENYCN 52
                                                                                      Chery Match
Best Local Similarity 59.39
Matches 51: Conservative
 25
57
96
33
43
116 AA;
                                  DISULFID
DISULFID
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CEAIN
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us-09-423-100-5.rspt

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091231 oncorphynchu
091162 oncorphynchu
09130 oncorphynchu
042336 myoxocephal
P81268 oncorphynchu
091965 oncorphynchu
091943 squalus aca
081943 squalus aca
08195 squalus aca
08195 squalus aca
08195 squalus aca
08195 squalus aca
08196 meleagris q
              08av14 petromyzon 09307 paralichthy 09320 oreochromis C42289 oreochromis P79824 oreochromis P79824 paralichthy 093527 paralichthy 0935161 oncorhynchic C91165 salmo salar 091475 salmo salar
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09pwk2 carassius a
098sr6 megalobrama
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Bukaryota, Motazoa, Chordata, Craniata, Vertebrata, Butelcostomi.
Nammalia, Butheria, Frimates, Catarrhini, Hominidae, Pongo.
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62.5%; Pred. No. 1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECTINGE FROM N.A.
Stead J.D.H., Jeffreys A.J.;
Stead J.D.H., Jeffreys A.J.;
"Haplotype diversity at the insulin region.";
Submitted (JUL-00814) at the EMBL/GenBank/JDbJ databases.
EMBL: AY13758: AAN05977.1;
SEQUENCE IIO AA, 12038 MW; 22D2B32B94F520F8 CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Q91162
Q91230
Q91965
Q911843
Q911E4
Q8MIE
Q8MIS
Q91380
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mes 52; Conservative
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Insulin precursor.
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Q91XI3
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JBHXV2
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Obixis spermoptela
OBwnw6 felis silvo
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                                                                                                                September 15, 2003, 11:54:30 ; Swarch time 27:31:4 Seronds (Williags all annexts) 669:520 Milliag coll spdates/seronds
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                                                                                                                                                                                                                               .....VEQCOTSTOSENGLENYON 52
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                                                                                                                                                                                                                                                                                                                                                         830525
              GenCole version 5.1.5
Copyright (c) 1993 - 2003 - Computer Ltd.
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                                                                                                                                                                                                                                                                                                                    830525 seqs, 258052604 residues
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0981A8
0981A8
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051X13
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Gapop 16.0 , Gapext 0.5
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1: sp_archea:*

2: sp_bacteria:*

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sp_phage:*
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Maximum DB seq length: 2600066300
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sp_rodent:*
sp_virus:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      I FVNORLGGSHLVEALYLVCGERGFFYTPKT----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Felis silvestris catus (Cat).
Bukaryota, Metazoa: Chordata, Craniata, Verrebrata, Suteleosromi.
Mammalia: Butheria; Carnivora: Fissipedia, Felidae, Felis.
                                                                                                                         Spermophilus tridecemlineatus (Thirteen-lind ground squirrel).
Ebkaryota, Metazoa: Ciordata; Craniata; Vertebrata; Eutelnostemi:
Hammalia; Eutheria; Rodentia; Sciuroquathi; Sciuridae; Sciurinae;
Spermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89,5%; Score 263: UR 11, Length 110:
50,3%; Pred: No. 3.6e 26:
170e :: Mismatches 0: indels 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4% Score 251: DB 6: Longth 119:
55.8% Pred. No. 1.6e-26;
dive 2: Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2000) to the EMBL/GenBank/EDS. databases.
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
INTERPRO: IPRO/0425; INSULIN/IGF/RELAXIN FAMILY.
FFGam; PF00049; Insulin: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4511768066228685 78064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 AA: 12069 MW: 95FB6E170C7BEDA4 CRC64:
01-DEC-2001 (TrEMBLrel. 19. Last sequence update) 01-MAR-2003 (TrEMBLrel. 23. Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last arnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FVNQHLCGSHLVEALY: VCGERGFFYTPKT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ALCKRGIVEGCCTSICSLYGLENYCN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RGIVECCESICSLYQEENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: 1PR004825: Ins/:GF/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS: PROCEZZ TRSCLINH.
SMART: SMOUOTS: 1.65. 1.
SMART: PSOCUEZZ: INSCLIN: 1.
SEQUENCE: 110 An: 12604 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLRel, 26, 01-MAR-2002 (TrEMBLRel, 20, 01-MAR-2003 (TrEMBLRel, 23, 01-MAR-2003 (TrEMBLRel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PR00277; INSULINE.
SMART; SM00078; ILGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.34
Whiches 51: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamoto S., Morimatsu M.; "cat insulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00049: Insulin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 48: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         NCBI_TaxID-43179;
                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preproimsulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Irwin D.M., Sivarajah P., "Proinsulin cDNAs from the leopard frog. Rana pipiens: evolution of proinsulin cDNAs from the leopard frog. Rana pipiens: evolution of proinsulin processing.", 1258:405-410(2000).

SIBCELINIAR LYGATION: SETRETED (BY SIMILARITY).

SIRCELINIAR LYGATION: SETRETED (BY SIMILARITY).

EMBL: SATIATION: ANY STREET AND THE INSULIN/IGF/RELAXIN PAMILY.

HSSP: POISS: 1SDB.
                                                                                                                                                                                                                                                                                                                                                     Rana pipiens (Northern Leopard frog).
Enkaryota: Metasca: Chordata: Craniata: Vortebrata; Euteleostomi:
Amphibia: Batrachia: Anura: Neobatrachia: Ranoidea; Ranidae: Rana.
NCB:_Tax1D-8404:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pantodon buchholtzi (Butterflyfish).
Eukaryota Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleoste; Osteoglossomorpha;
Steoglossiformes; Pantodoctidae; Pantodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=2120357; PubMed-11306171; AL-Mahrouki A.A., Trwin D.M., Graham L.C., Youson J.H.; Al-Mahrouki A.A., Trwin D.M., Graham L.C., Youson J.H.; Molecular clonding of preproinsulin cDNAs from several exteoglossomorphs and a cyprinid ": Mol. Cell. Endocrinol. 174:51-58(2001).
-!-SUBCELLUIAR LOCATION: SECRETFO (BY SIMILARITY).
-!-SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL: AF195588 ARA28712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FVNOHLCGSHLVEALYLVCGERGFFYTPKIR----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12183 MW; 3A870EEC70217F92 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74,7%; Score 219.5; DB 49.4%; Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 AA
                                                                                                                                                                                                  106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7: Mismatches
01-00N-2001 (TrEMBLICAL 17, Created)
01-00N-2001 (TrEMBLICAL 17, Last sequ
01-MAR-2003 (TrEMBLICAL 23, Last anno
                                                                                                                                                                                                                                                 01-001-2000 (TrBMB1rel, 15, Created) 01-001-2000 (TrBMB1rel, 15, Last seq 01-MAR-2003 (TrBMH1rel, 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 KPGIVEQCCHNTCSLYDLENYCN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 -- GIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diterpro, TPR00482; Ins/ISF/relax.
Pfar: PP60049; Insulin: 1
PAINTS: PR0277; INSULINS.
SMART; SM0028: IIGF: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
MEDLINE-20362507; PubMed-10818274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSTITUTE 1
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Best Local Similarity 49.49
Matches 41; Conservative
                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PSOC262;
SECUENCE 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_faxID=8276;
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Tue Sep 16 08:22:54 2003

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4 QHI.CGSHLVEALYLVCGERGFFYTPK -----T 30
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Actinopterygii, Neopterygii, Teleostoi, Ostariophysi: Cyprinitormes:
Cyprinidae, Catla.
                                                                                                                                                                                                                                                                                               Chitala chitala (clown knifefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bokaryota; Meoptoryqii; Teleostel; Ostcoglossomorpha;
Osteoglossiformes; Natopteridac; Chitala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.5%; Score 195.5; DB 13; Length 108; 45.1%; Pred. No. 5.8e-19; tive 5; Mismatches 7; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, PS00262: INSULIN; 1.
SEQUENCE 108 AA; 11881 MW; D713026E22EF5D59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (ITEMBLIEL. 17, Greated)
01-JUN-2001 (ITEMBLIEL. 17, Last sequence update)
01-RAN-2003 (ITEMBLIEL. 23, Last annotation update)
Preproinsulin (Fragment).
     ol DEC-2001 (TrBMBLTCL, 19, Created)
03-DEC-2001 (TrBMBLTcl, 19, Last sequence update)
01-MAR-2003 (TrBMBLTcl, 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 RGIVEQCCTSICSLYOLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 45.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.2
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY:
                                                                                                              Catla catla (catla)
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                           NCBI_TaxID-72446;
                                                                                           Preprofusulin.
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Q987B0;
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Eukaryota: Metazoa: Chordata: Granlata: Vertebrata: Euteleostori:
Actinopteryqui: Neopteryqui: Teleostei: Ostariophysi: Cyptiniformes:
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Argenton F., Zoecoln. B., Nortolussi M.;
"Early appearance of pancheatic hormone-expressing cells in the zebrafish embryon":
"Farly appearance of pancheatic hormone-expressing cells in the mech. Dev. 47:217-22(1999).
"I SUBCELLUSAR LOCATION: SECRETED (BY SIMITARITY).
"I SAMILARITY: SECONDS TO THE INSUIN/IGF/RETAXIN FAMILY.
HSSP: PO1308: 11291.
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                                                                                                                                                                  Query Match 68.5%; Score 201.5; DR 1%; Longih 110;
Best Local Similarity 43.5%; Prod. No. 9.30-20;
Matches 57; Conservative 8; Mismatches 9; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indes
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                                                                                                            12324 MW: HDECCD6590872806 03064:
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Last annotation update)
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45.1%; Pred, No. 5.80~1%;
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INSULTN B CHAIN.
INSULTN A CHAIN.
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                                                                                                                                                                                                                                                                              3 NOHLCGSHLVEALYLVCGERGFFYTPKT - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                       86 KVKRGIVEQCCHHPCNIFPLONYCN 110
                                                                                                                                                                                                                                                                                                                                                                                       31 --- RGIVEQUETSICS / YQLENYON 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last Seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
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InterPro: IPR04825; Ins/:GE/rolax.
Pfm: FP00349; Insulin: 1.
PR:WTS: PR00227; INSULINS.
SWART: SW00378: 11GF: 1.
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InterPro: IPRO04625; Ins/ISF/relax. Perm: PRO049; Institut 1. SMARP: SW0078: ILUS: IPROSITE: PROSITE: PSCC262: INSULIN: I.
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86 108 11
108 AA: 11904 MW:
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                                                                                                            110 AA;
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Matches 37: Conserv
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0902N4;
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CHAIN
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Q902N4
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Prints: PROCO49: Insuling a Prints: PRINTS; PROCO77; INSULINB. SMART; SM00078: 11GF: 1. PROSITE: PSOCO52; INSULIN: 1.
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PROSITE; PS00262; INSULIN; 1.
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Best Local Similarity 42.9
Matches 36: Conservative
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                26 SQHLCGSHLVDALYMVCGEKGPFYQPKTKRDVDPLLGFLSPKSAQENEADEYPYKDGGDL 85
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 10, Last annotation update)
Preproinsulin (Fragment)
Preproinsulin (Fragment)
Csteoglossum bicirrhosum (silver arawana)
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Enteleostomi:
Actinopterygii; Neopterygii; Teleostei: Ostcoglossomorpha;
                                                                                                                                                                                                                                   Hiodon alesoides (goldeye).
Bukaryota, Metazca, Chondata, Crantata, Veitelrafa; Etheleoston.:
Actinoptorygii, Neopterygii; Teleostei; Geteoglossonorpia;
Osteoglossiformes: Hiodontidae: Hodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.8%: Score 193.5; DR 13: Lonath 110: 42.4%; Fred: No. 1.1e-18; Live 7; Mismatches 7; Indels 35;
                                                                                                                                                                                                                                                                                                                  P SEQUENCE FROM N.A.

X MEDIZEE-21203577; Pubmed-11306171;
MAI-Mahrouxi A.A.; Irwin D.M.; Graham L.C.; Youson C.H.;
T decender cloning of preproducing in consecutive cloning of preproducing in consecutive cloning of preproducing in consecutive cloning of preproducing in cost cool ossemorphs and a cyptinid.";

MOI-GELL Endocrinol. 174:51-58(2001).

1 MOI-GELL CARCALICAR NOCALICAR SECRETED (BW STMILARITY).

C -1 STMILARITY: HELDNIS TO THE INSULIN/OFFFEIANIN FAMILY RESP. POI-308; ILM.

EMBL. AP282478; ARS44684.1;
RESP. POI-308; ILM.

RESP. POI-308; ILM.

RESP. POI-0099; TANILLO. 1.

PRINTS: PREG0277; INSULINE.

PRINTS: PREG0277; INSULINE.

PRINTS: SMC0079; ILM.

SMRRI: SMC0079; ILM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21203577: Pubxed-11306171:
Al-Mahrouki A.A., Irwin D.M., Shaham L.C., Youson J.H.,
"Molecular conting of preproinsulin coNAs from several
osteoglossomorphs and a cyptrinid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 AA: 12343 WW, BDECCD7703852808 ORC64;
                                                                                                                                                                             61-DEC-2001 (TrEMBirel, 19, Created)
01-DEC-2091 (TrEMBirel, 19, Last sequence update)
11-MAR-2093 (TrEMBirel, 23, Last annotation update)
Preprojection (Pragment)
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3 NOHLOGSHLVEALYLVCGERGFFYTPK -----
                                                                                 VKMKRGIVEQCCHRPCNLFDQNQYCN 111
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tes 36; Conservative
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27 SQRLCGSHLVDALYMVCGDRGFFYSPKSRREAEFLLGFLSPKSGQENEVDEYPYKEQGEL 86
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Actinopteryqii: Neopteryqii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Gnathonemus.
                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                                                                                                                                                                                                                                                                         Ouery Match 65.1%; Score 191.5; DB 13; Length 111; sest Local Similarity 41.2%; Pred. No. 2.1e-18; Matches 35; Conservative 16; Mismatches 5; Indels 35;
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Mol. Cell. Endocrinel. 174:51-58(2001).
-!- SUBCELLCLAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL: AF195389; AAK28713.1; -.
HSSP; P01315; IMPJ.
InterPro: IPR004825; I::s/IGF/relax.
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"Molecular clonking of preproinsulin cDNAs from several
esteoglossomorphs and a cyprinid.";
Mol. Call. Endocrinol. 774:51-58(2001).
-:- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-:- SIMILARITY: HELCOGY TO THE INSULIN/IGF/RELAXIN FAMILY.
FMBL, AR199587: AAK2871:.1;
HSSP; F01308: 1HIS.
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42.9%; Pred. No. 5.8e-18; ....marrhes 8; Indels
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SEQUENCE 111 AA: 12491 MW; AC9E19D2D4866D20 CRC64;
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01-30N-2001 (TEMBEROL 17, Greated)
01-30M-2001 (TEMBEROL 17, Last Sequence update)
11-MANE-2003 (TEMBEROL 23, Last ancotation update)
9reprolestin (Fragment).
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Ffam: PF00049; Insulin; 1.
SMART: SMC0078; IIGF; 1.
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Gaps

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SEQUENCE FROM N.A.
O'Migin C., Tichy H., Klein J.;
Molecular evolution in higher primates: gene specific and organism specific characteristics.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY092023; AAM76640.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE FROM N.A.
C'INIGAIN C., TICHY H., Klein J.;
C'INIGAIN C., TICHY H., Klein J.;
Wholecular correction in higher primates; gene specific and organism specific characteristics.";
Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases.
BMBL, AY092024; AAM75441.1; -..
NON_TER 65 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
NCBI_TaxID-9593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Pongo.
         Sength 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 146; DB 6; Length 65; Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; indels
                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B772017FD8BCABEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G1-MAR-2003 (TrEMBLrel, 23, Created)
G1-MAR-2003 (TrEMBLrel, 23, Last sequence update)
G1-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OL-MAR-2003 (TFRMELRE). 23, Created)
OL-MAR-2003 (TFEMELRE). 23, Last sequence update)
Cl-MAR-2003 (TFEMELRE). 23, Last annotation update)
         DB 13;
Score 185.5; DB 13;
Pred. No. 1.1e-17;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CGSHLVEALYLVCGERGFFYTPKT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                    4 OBLOGSHLVEALYLVCGERGFFYTPK-----
                                                                                                                                                                                                                                                                                                                                                      30 ----IRGIVEQUOTSICSLYOLENYON 52
                                                                                                                                                                                                                                                                                                                                                                                                                                            64 MEMMYKRGIVEOCCHHPCNIFDLGRYCN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 AA; 6920 MW;
         63.285
40.985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.78:
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64.17
Sest Local Similarity 46.97
Marches 46, Couservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorilla gorilla (gorilla)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 47.7
es 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRED : MINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin (Fragment)
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SEQUENCE
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Sest focal S
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088280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 QHLCGSHLVDAJYLVCSPTGPPYNPKRDVHALISHJPPKSSPENBVADFAFKDHAELLEK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sapp
                                                                                                                                                                                                                    Preproinsulin (Fraqment).
CatoStomus commersoni (White sucker).
Eukaryota; Matazoa: Chordata, Craniata; Verrebrata: Buteleostomi,
Actinopterygii; Neopterygii; Teleostami; Ostariophysi; Syptinitormes:
CatoStomidae; CatoStomus.
NCBL_FaxID=7971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preproinstill (Frammers) and manuality update)
Ambieplites rupestile (Framment).
Eukaryota: Metadoa: Chordata: Graniata; Verfebrata: Eutoperstock:
Actinopierygi: Neoptergqi: Telecatei: Eutofesstei: Neoptergdi: Telecatei: Eutofesstei: Neoptergdi: Centrarchidae; Ambieplites: Neoptergdi: Percomorpha: Dereffermes: Ferricle:
NCBL_TAXID-109273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 186.5; DB 13; Length 108: Pred. No. 9.8e-18; 4; Mismatches 9; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MENTINE-2120'5577; PubMed'1110'6171;

An-Mahrouki A.A., Jrwin D.M., Graham D.C., Youson J.H.;

An-Mahrouki A.A., Jrwin D.M., Graham D.C., Youson J.H.;

Molecular clonique of preproinsulm cukhas from several costcopiossomorphs and a cyptinid.":

Mol. Cell. Endocrinol. 174:51-58(2001).

C. !- SUBCELULAR COCATION: SECRETED (BY SIXILARITY).

C. !- SUBCELULAR COCATION: SECRETED (BY SIXILARITY).

R. PRESP. PO1308: Law.

R. HASB. PO1308: Law.

R. HASB. PO1308: Law.

R. FASB. PO1308: Law.

R. FASB. PO1308: Law.

R. FASB. PO1308: Law.

R. PROCAGO, INGULAL I.C.

R. PROCAGO, I.C.

R. PROCAGO, INGULAL I.C.

R. PROCAGO, I.C.

R. PROCAGO, INGULAL I.C.

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R. PROCAGO, I.C.

R. PROCAGO, INGULAL I.C.

R. PROCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E426310696FBAF08 CRC64;
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01-00N-2001 (TrEMHLRE), 17, Last sequence update)
01-MAR-2003 (TrEMHLRE), 28, Last annotation update)
                                                                                     01-JUN-2001 (Tremmirel, 17, Greated)
01-JGN-2001 (Fremmirel, 17, Last sequence update)
01-MAR-2003 (Tremmirel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 43
         178 A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR054825; Ins/IGF/relax.
Pfam: PF30049; Insulin; 1.
SMART; SM06078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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    FRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 AA;
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SEQUENCE
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098TB2
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Gaps

34;

Best Local Similarity 47.7% Pred. No. 2e 12: Matches 31; Conservative C; Mismatches	al Simil 31: C	arity Onserva	47.78 tive	Pred. C; Mi	Pred. No. 2e 12 C; Mismatches		- 1	0; Indels		sans	
٥٧	7 CGSH	LVEALYL	7 CGSHLVPALYLVCSSRGFPYTPKT	FYTPKT-		1				: ::::::::::::::::::::::::::::::::::::	
	1 CGSH	LVEALYI	COSHLVBALYLVCGERGFFYTPKTRREAEDLQVQQVELANGPSAGSLDFFALESSTOKKG 69	FYTEKTR	REAEDIG	VGQVET	:555:	GAGSLOF	SUSTRU	TOKAS 6	.=
0y	33 IVEQ	IVEQC 37									
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Search completed: September 15, 2003, 12:03:30 Job time: 21:3154 secs

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Genfore version 5.1.6
Copyright (c) 1993 - 2003 - Compuges
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using sw model protein search, OM protein

September 16, 2003, 12:33:20 ; Search time 3,542 Seconds (without alternate) 536.746 Million cell updates/sec Run on:

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Title: Perfect so Sequence:

US-09-423-100-6 587 score:

1 MEPTIFUSRIFONAMIRAHR. Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 3.5

1107863 seqs, 158726573 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seg leugth: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

•• Database

/SIDSI/gcgdata/geneseq/geneseqp-cmbl/AA1980.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-cmbl/AA1981.LAT:*/SIDSI/gcgdata/geneseqp-cmbl/AA1982.LAT:* A_Geneseq_19Jun03:*

75.1031/gcddata/geneset/genesetp-emb1/AA194 1.071.
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/SIDSI/dogdata/geneseq/genesegp.empl/AA2502.Lat:*/SIDSI/geqdata/geneseq/genesegp.embl/AA2903.Lat:*

Prod. No. is the number of results producton by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	The control of the second of t	Chimeric protein.	SOB-projusajin jun	Heman pro-insulin	SCO-profession ave	Mating factor alph	Human pro-insulin	Proinsilin sequenc	Human pro-institu
	g:	AAY42850	AAY42861	AAR98857	AAR68300	AAR98896	AAR71692	AAR68901	AAR78665	AAR58899
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	Query Match Length DB ID	100.0 107 20	150	315	63	1117	137	yo Vo	36	96
æ	Ouery Match	150.0	94.6	53.7	51.8	87.5	51.5	50.9	50.9	50.9
	Score	587	555.5	315.5	304	304	302.5	568	299	562
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Fusion protein con Mating factor alph Mating factor alph Human insulin prec Proissulin analoqu	Glyccsylphosphatid Example of human i Preproinsulin 1. pKV142 modified in Modified physty mod	N-terminally exten N-terminally exten Amino acids encode EEAEPK-WI3 insulin DNA construct pAK7 PAK855 protein seq SANTHALIC leader b	Insulin precursor EEAEPK-MIS insulin Amino acides encode S. cerevisiae MF a Mating factor alph Mating factor alph Ui-Arg-(B31-32)-Hu Insl double-chain	Protein sequence o A Bacillus pectate Aunino acids encode EEAEPK-MII insulin Human proinsulin a Aunino acids encode Human preproinsuli Signal leader-p-in Yeast signal/leade Sequence encoded b Signal peptide/lea
			ABP55059 AAM19242 AAP9643 AAM04890 AAR71693 AAR5883 AAM18607	4, 4,
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AL, I CNMENTS

AAY42860 standard; protein; 107 19-JAN-2000 (first entry) AAY42860; RESULT 1 AAY42860

AA.

hdH-mini-proinsulin chimeric protein.

Insulin, precursor, growth hormone, chaperone, intramolecular; folding, conformation, chimeric protein, cleavable, recombinant, production, yield.

Scapiers occi Synthetic

W09950302-A1

07 OCT-1999.

98WO-CN00052 31-MAR-1998; (TONG-) TONGRUA GANTECH BIOTECHNOLOGY LID.

98WO-CN00052

41-MAR-1998;

Gan 2;

WFI; 1999-610839/52.

New chimeric proteins containing human growth hormone fragment, used

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AAR98897
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                                                                                                                                                                                                                                                                 the fusion proteins, thus allowing folding of the fused institutions at commercially useful high concentrations. The procedural steps of expanagen bromide cleavage, oxidative sulphitritysis and related to purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent essins.
                                                 This sequence represents a chimeric protein, hGH-mini-prolinguille.
This chimeric protein contains an N-terminal fraqment of human growth hormone (hGH) of the sequence given in ANY42855, a sleavable peptide linker (ANY42857), and a human insulin precursor comprising insulin A and B chains (ANY42859). The hGH portion of the chimeric protein acts as an intramolecular chapterone (LMC) for the insulin precursor, enabling it to fold correctly. The cleavable peptide linker has a C-terminal Arg residue which enables the hGH portion of the chimeric protein to be removed after folding has taken place. Production
                                                                                                                                                                      of recombinant human insulin via an hoH-proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher viola of human insulin. The IMC sequences not only protect insulin sequences from intracellular decradation by a micrororganism host, but also provide the folding of the fused insulin precision: familiar time solubility of the fused insulin precision. Additional additional and decrease the intermedental interactions among the fusion protein and decrease the intermedental interactions among
                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric proteins containing human growth hordone fragment, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulio: precursor; growth hormone: chaperone; intramolecular;
folding; conformation; chimeric protein; cleavable; recombinant;
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100.0%: Pred. No. 46-42;
Live 0; Mismatches 10: Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LCGSHLVEALYLVCGERGFFYTPKTRGIVEGOOTSICSLYGJENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  particularly for the production of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY42861 standard; protein: 150 AA.
                           Claim 13; Page 30; 46pp; English
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                  107
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This sequence represents a chimeric protein, which contains an N-terminal fragment of human growth hormone (hGH) of the sequence given in AAX42856, a cleavable peptide linker (AAX4285), and a human insulin precursor comprising insulin A and B chains (AAX42859). The HGH portion of the chimeric protein acts as an intramplecular chaperone (IMC) for the chimeric protein acts as an intramplecular chaperone (IMC) for the chimeric protein acts as an intramplecular chaperone (IMC) for the chimeric protein at a C-terminal Arg residue which enables the hGH portion of the chimeric protein to be removed after folding has taken place. The chimeric protein to be removed after folding has taken place or protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher protein of human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher sequences from intracellular degradation by a microorganism host, but also promote the folding of the fused insulin precursor, facilitate the solubility of the fusion protein and decrease the intermolecular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions among the fusion proteins, thus allowing folding of the first insulin precursor at commercially useful high concentrations. The procedural steps of opening bromide cleavage, oxidative sulphitolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptam or the use of hydrophobic absorbent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1) TESNKEETQQKSNEELLRISILLIOSMLEPVQLGTGPRFVNQELGGSHEVEALYLVGGBR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 150;
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particularly for the production of human insulin
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ive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 GFFYTPKTRGIVEQUCTSICSLYQLENYON 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BICT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                     Claim 14: Page 30-31; 46pp: English.
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95ZA-0000142.
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es 107; Conserv
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with a rereaptan to provide 2-10 SH residues per Cys residue, in presence of a charterpic agent and in ag. medium of pH 10-11.

Treating the proof with 3-50 g hydrophobic adsorber resin per i ag. medium of pH 4-7, isolation, the adsorbed resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with Known methods it involves fewer stages (egs. no sulphitolysis or cyanogen bromide cleavage) and overall losses during purification are reduced, i.e. the process is quicker and gives better yields.

Sequences of insulin chain A, B and C are given in AAR68895-97.

Sequences of finsulin -4 are given in AAR68898-901.
                                                                                                                                                                                                                                                                                                                                                                                                               51 GTGPRFVNQHLGGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GNSARFVNORLGGSBLVEALYIVCGERGFFYTFKTRGIVEGCCTSICSLYQLENYCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises folding a hybrid polypeptide comprising proinsulin under conditions that permit correct disulphide bond formation and subjecting that folded procein to enzymatic cleavage. The insulin produced can then be purified. This sequence is a SOD-insulin B chain-Lys-Arg-insulin B chain-Lys-Arg-insulin B chain hybrid polypeptide and is encoded by the plasmid construct pBAST-R. Transformation of the proper E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant insulin prodo, by correctly folding pro-insulin hybrid polypeptide - then enzymatic cleavage of folded product, does not require sulphite protection of SH nor use of cyanogen bromide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new method for the production of recombinant human insulin
                                                                                                                                                                                                                                                                                                                                           51.8%; Score 304; DB 15; Length 63; 94.7%; Pred. No. 1.3e-18; ive 0; Mismatches 3: Indels
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                                  Disclosure: Page 11-12: 15pp: German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example LA: Figure 6; 69pp; English.
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es 54: Conservative
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                                                Recombinant insatin produ. To correctly folding pre insulfic hypolopolypoptide - Then enzymatic eleavage of tolded product, does not require salphite protection of SB not use of eyanosen browide.
                                                                                                                                                  A new method for the production of recontinant human invitin comprises folding a hybrid polypepilde comprising profitsuit inder conditions that permit correct disalphide bond formation and subjecting that folded protein to englighte cleavage. The insulin produced can then be purified. This sequence is a SCD-insulin Behain-ray insulin A chain hybrid polypepilde and is encoded by the plasmid construct poBASC-LAT. Transformation of the properties to the profitsuit hybrid polypepilde and is encoded by the profit of the profit hybrid polypepilde. Wastel for human insulin production. The method produces recombinant human insulin identical to the natural hommone. Hazardous and cumbersome
                                                                                                                                                                                                                                                                                                                                           procedures involving eyanogen bromide and suiphitolysis to protect SH groups are avoided since the entire hybrid polypoptide folds efficiently to the native structure even with the leader attached
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e5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 315.5; DB 17; Length 116;
Pred. No. 2.5e<sup>-</sup>19;
2; Mismatches 5; indeis 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro-insulin, A chain, B-chain, C-chain: disulphide:
mercaptan; chaotropic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 5e<sup>-</sup>297
Pes 5<sub>7</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sabe: W;
                                                                                                                     Example 18: Figure 7: 69pp: English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR68900 standard; peptide: 63 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.78
85.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.3
Matches 58, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003 (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 YULENYCH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 YOLENYON 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human pro-insulin 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 1994-177718/22.
WPI: 1996-333766/33
                                                                                                                                                                                                                                                                                                                                                                                               and Cys unprotected
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                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA;
                   N-PSDB; AAT34670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NCV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C2-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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Gaps

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Length 137;

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:8 STNNGLLFINTTIASIAAKEEGVSMAKREVNQHLCGSHLVEALYLVCGEKGFFYTPKTRG 117
                                                                                                                                      3 FPS1-----FTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSN
                                                                                                                                                             49 PLGTG--------PRFVNOHLCGSHLVEALYLVCGERGFFYTPKTRG
 A20/B19. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for diabetes (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                2 FPT1PLSRLFUNAMLRAHRLHQLAFDTYQEFFEAYIPKEU--KYSFLQ-
                                                                            3.6e-18;
hes 27; Inders
                                                                     DB 16;
                                                                                          4; Mismatches
                                                                    Score 302.5;
Pred. No. 3.6
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                                                                                                                                                                                                        Obermeier R,
                                                                    51.5%;
50.0%;
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                                                                                                                                                                                                                                                                                     AAR6890] standard; peptide;
                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                    Human pro-insulin 3.
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                                                                            Local Similarity
es 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARH ) HOECHST AG
                                              137 AA;
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02-MAR-1995
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                                                                 Chery Match
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                                                                                           Matches
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                                                                                                                                                                                                                                                                                                    43 YSPLONPLOT - - GPREVNUHLOGSHIJVEALYLVOGERGFFYTPKT - RULVEQCCTSLOS 98
                                                                                                                                        80.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQB6425 encodes AAR71692 mating factor alpha Finsulin precusor ArgB1. ArgB1 comprises the B and A chains of a claimed buran insulin derivative. In the final claimed compen. they are covalently connected via disulphide honds between Cys residues AVAP7 and
host cells with pBAST-R results in the efficient expression of the profusulin hybrid polypeptide, useful for buran insulin production. The method produces recombined human insulin identical to the natural hormone. Hazardous and cumbersome procedures involving expangen bromide and sulfahitolysis to protect SH groups are avoided since the entire hybrid polypeptide folds efficiently to the native structure even with the loader altached and Tys unprotected.
                                                                                                                                       -.r
                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                       Human insulin precursor ArgB31; diabetes; Zinc Lon complex; mating factor alpha :.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acylated insulfu doriv, which may be present as a zinc be complex of is used to treat diabetes and is rapid acting.
                                                                                                                                      5: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jonassen
                                                                                                               51.8%; Score 304; DB 17:
82.6%; Pred. No. 2.3e-18:
                                                                                                                                                                                                                                                                                                                                                                    Mating factor alpha 1-Insulin precursor Argisl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- mating factor alpha-1
                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualitiers
1..85
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                                                                                                                                                                                                                                                                                      AAR71692 standard; Protein: 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     set Broheim
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94US-0190823.
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                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                           Best Local Similarity 82.6
Matches 57: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86...116 / Zlabel: 3
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                                                                                                                                                                                                         DYOLENYCK 107
                                                                                                                                                                                                                     109 EYOLENYON 117
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                                                                                         117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1994;
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20-NOV-1955
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                                                                                           Sequence
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5
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ID AAR7
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Pro-insulin is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in preeded agent and in aq. medium of pH 10-11, irecting the prod. with 3-50 g hydrophobic adsorber resin per 1 aq. medium of pH 4-7, isolating the adsorbed resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin and correctly bonded Cys bridges. Compared with known methods it involves fewer stages (esp. no sulphitolysis or cyanogen bromide the process is quicker and gives better yields.

C Sequences of insulin chain A, B and C are given in AAR68895-97.

Sequences of pro-insulin 1-4 are given in AAR68898-901.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating recombinant precursor protein with morcaptan in alkali
and in presence of chaotropic agent, then isolation on
hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of pro-insulin with correct dissulphide bridges -
Fro-insulin: A-chain: P-chain; C-chain; disulphide;
mercaptan; chaotropic agent.
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Gaps 107

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98

g

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Profitable 1s produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in presence of a chactropic agent and in act medium of pH 10-11, treating the produce produce produce produce the produce the produce of a hydrophobic adsorber resin per medium of pH 4-7, isolating the adsorber resin and profits per medium of pH 4-7, isolating the adsorber resin and desorbing the profitsulin. This method produces profitsulin with correctly bonded Cys bridges. Compared with known methods it involves fewer stades (sep. no sulphitclysis or cyanogen bromide of the process is quicker and gives better yields.

Sequences of insulin chain A, B and C are given in AAR68898-97.

Sequences of profitsulin the given in AAR68898-901.

(Updated on 25-MAR-2003 to correct PN field.)
bridges. Reaction with trypsin and opt. carboxypeptidase B yields correctly folded insulin. The insulin is isolated by absortion on a hydrophobic resin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Produced pro-insular with correct dissulphide bridges - by treating recombinant procursor protein with mercaptan in alkaliand in presence of chaotiopic agent, then isolation on
                                                                                                                                                                                                                                                      55 REVNOHIGGSHIVEALYINGERGEFYTPKTRGIVEGGGTSICSLYGLENYCN
                                                                                                                                                                                                                                                                                   4. REVNOHIGGSHIVEALTINGGERGFEYTPKTHGUTINGGCTSICSLYQLENYCH
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                                                                                                                                                    Leng: h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Provinsulu, A-chain, B-chain, C-chain, disulphide, mercaptan, chaotropic agent.
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                                                                                                                                                                                                         ċ
                                                                                                                                                       Score 299; DB 16;
Pred. No. 3.2e-18;
                                                                                                                                 50.5%; Scor.
105.5%; Pred. No. c.
0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR68899 standard: peptide; 96 AA
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                                                                                                                                                                                                         53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pro-insulin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serl M, Ludwig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WP1: 1994-177718/22
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                                                                                                                                                                               Similarity
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                                                                                                    56 AM:
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02-MAR-1995
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                                                                                                       aonombos
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                                                                                                                                                                               Hest Legal
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
AARE8899
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                                                                                                                          The present sequence is an example of a preinsulin molecule near sequence to the general formula R2-F1-(R2-R39) V-X-5(Y-CA2-A20)-F3 (11). Informula (11), X - 159. Arg or a peptide of 2-15 amino acids nontal bys or Arg at the N-son Greenini V- a natural amino acids nontal phe or a bond; R2 - H, Ara, Lys, a peptide of 2-45 amino acids contal order Ara, Lhe N- and G-termini V- a natural amino acids contal Ara, CA2-A20, and the N-son acids and contant Arab (A2-A20) and (R2-R1) Arab G-15 and G-15 amino acids (A2-A20) and (R2-R1) Arab G-15 and G-15 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolation of insulin that is correctly post translationally processed - by reacting preciming with a mercaptan in the presence of a chaotropic agent and purifien, after absorption to hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proinsuling post-translational modifications recombinant productions
                                                                                                                                                                         55 REVNOHLOGSHIJVEALYIJVGGBRGFEYTEKTRGIVEGGGISTGSLYG; ENYGN 1 7
                                                                                                                                                                                                      ::
                                                                          Length 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noter "a peptide of 4 amino acids"
                                                                          Spore 299: DB 15:
Pred. No. 3.2e-18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sote- "human issulin B-chals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36..56
/label- Gly-(A2-A20)-83
/note= "human insalin A-chain"
                                                                                          160,0%: Pred. No. 3.2
ive 0: Mismalches
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                                                                                                                                                                                                                                                                                                                                                      AAR78665 standard: protein: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein folding; conformation.
                                                                          50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95EP-0101748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proinsulin sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-284754/38.
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                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARH ) HORCHST AG
                          A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1996
                                                                       Ouery Match
Best Local Simi
Matches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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ö Gaps 55 REVNOHICGSHIVEALYLVCGERGFFYTPKTRGIVEQUCISICSLYQLENYCN 107 Ċ <u></u>

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which contains an example of a profession molecule correspond to the general formula R2-R4. (B2-B25)-TX-Giy-(A2-A20)-R3 (11). In formula (11), X = Lys. Arg or appetite of 2-55 amino acids contage to Arg at the N- and C-remini; Y • a natural amino acid; R1 = C Phe or a bond; R2 = H, Arg. Lys. a peptide of 2-45 amino acids contage. Arg or Lys at the N- and C-termini; R3 • a natural amino acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequence acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequence from human or other Insulin. The profusulin molecule, released by cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 Si residues of mercaptan per Cys residue of profusulin. The reaction: C takes place in the presence of a chaotropic auxiliary agent at PH 10-11 and results. In profusulin with correctly linked cystine or bridges. Reaction with trypsin and opt. Carboxyperidates Bysician correctly folded insulin. The insulin is isolated by absortion on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolation of insulin that is correctly post-translationally processed - by reacting pro-insulin with a mercaptan in the prosence of a chaotropic agent and purifice, after absorption to hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                  Proinsulin; post-translational modification; recombinant production; protein folding; conformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is that of a fusion protein, produced in E.coll
| USE | UTILITY | UTILITY | USE | UTILITY | UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "a peptide of 4 amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B-chain"
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                                                                                                                                                                                                                                                                                                                                                             Fusion protein contg. proinsulin sequence
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/note+ "human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                        AAR78662 standard; protein;
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/label- R2
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a hydrophobic resim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARH ) HOECHST AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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of a chaot
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                                                                                                                                                                                                                                      AAR78662;
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Region
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Score 299; DB 16; Length 96;

50.9%;

Query Match

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                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ86429 encodes AAR71694 mating factor alpha 1-Insulin precursor ArgB1, ArgB1 N-terminal EEAEAEAR. The insulin precursor comprises the H and A chains of a claimed human insulin derivative preceded by the N-terminal amino acids EEAEAEAR. In the final claimed compsn. they are covalently connected via disulphide honds between Cys residues A7/B7 and A20/B19. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                          55 REVNOHIGGSHIVEALYLVGGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                               precursor ArgBl, ArgB31: diabetes; Zinc ion complex; alpha 1: N-terminal EEAEAEAR.
                                                      44 REVNQHLGGSHLVBALYLVCGERGFFYTPKTRGLVEQCCISICSLYQLENYCN 96
                                                                                                                                                                                                                        Mating factor alpha 1-Insulin precursor ArgB1, ArgB31 N-terminal.
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                 indels
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100.0%; Pred. No. 5.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 299; DB 16;
Pred. No. 7.3e-18;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    abel - mating factor alpha-l
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/label- N-terminal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Pages 82-83; 100pp; English.
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                AAR71694 standard; Protein; 145 AA
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100.0%; Pro
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/label- B-chain
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/label- A-chain
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94US-0190829.
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                                                                                                                                                                                   (updated)
(first entry)
Best Local Similarity 100.3
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guery Match
Best Local Similarity 100.
Matches 53, Conservative
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N-PSDB: AA086429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AA;
                                                                                                                                                                                                                                               Human insulin
mating factor
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MO9807931-A1
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                                                                                                                                                                                 25-MAR-2003
20-NOV-1995
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                                                                                                                                                        AAR71694;
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Frotein
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conformation: chimeric protein; cleavable; recombinant;

98WO-CK00052 98WO-CN00052

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New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin
                                                                                                                                     institut precursor; growth hormone; chaperone; intrampleular;
                                                                                                                                                                                                                                                                                                                        (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
                              AAY42659 standard: protein; 52 AA.
                                                                                                           Homan insulin precorsor, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-610839/52.
                                                                                                                                                               production: yield.
                                                                                 9-JAN 2000
                                                                                                                                                                                                                 WC9950302-A1
                                                                                                                                                                                                                                                                     31-MAR-1998;
                                                                                                                                                                                                                                                                                              31-MAR-1998;
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                          .9991-T00-T0
                                                       AAY42859;
    RESULT 13
                 AAY42950
                                            ArgBl. ArgB31 N-terminal EDASAEABN. The insulin precursor comprises the B and A chains of a claumed bumen insuling destinative for co-doct by the N-terminal amino acids REARAMER. In the final claimed roungs, they are covalently connected via disulphide behaves the
precursor Andil, Arghill dissers; Zinc les somplex; alpha ); N-terminal EEAEASAFK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues AZ/B7 and AZB/H15. The derivative, which may be present as a zinc ton complex, can be used as a fast action treatment tot diabetes.
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                                                                                                                                                                         Mating factor alpha 1-Insplin precursor Argsl, Aras31 N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acylated insulin deliv, which may be present as a Zinc Ton complex - is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jonassen I;
                                                                                                                                                                                                                                                                                             mating factor alpha-1
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Zabel- N-terminal peptide
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                                                                                                                                                                                                                                                                  Socation/Qualitiers
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                                                                               AAR71695 standard; Protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                /label* B-chain
                                                                                                                                                                                                                                                                                                                                                                        /label- A-chain
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                                                                                                                                                 (:irst entry)
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label
                                                                                                                                    (updated)
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N-PSDB; AAQ86432.
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                                                                                                                                                                                                  Human insulin
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Markussen J;
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20-NOV-1995
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                                                                                                        AAR71695;
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               6
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                                                       RESULT 12
AAR71695
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This sequence represents a human insulin precursor comprising insulin And Bechins. This insulin precursor is a component of the chimeric proteins And Bechins. This insulin (And 2086) and the chimeric protein and given in AND 42861. These chimeric proteins additionally contain an N-terminal fragment of human growth hormone (hGH) and a cleavable peptide linker (AND 4887). The hGH portion of the chimeric protein acts as an intrample cular chaperone (HMC) for the insulin precursor, enabling it to fold correctly. The cleavable peptide linker has a climeric protein to be removed after folding has taken place. Production of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin via an hGH-proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The INC sequences not only protect insulin sequences from intracollular degradation by a microorganism host, but also promote the finsion proteins and decrease the intermolecular interactions among the fusion proteins. This allowing of the insulin precursor. The fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the fusion proteins, this allowing folding of the fused insulin precure at commercially useful high concentrations. The procedural steps of cyanocen bromide cleavage, oxidative subhittolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 FVNQHIGGSHLVEALYLVGGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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Pred. No. 7.8e-18;
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Claim 12; Page 29-30; 46pp; English.
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100.0%; Pre
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50 9%; Score 299; DB 16; Lonath 146; 100.0%; Pred. No. 7.48-18;

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Mismate::es

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Conservative

Local Similarity nes 53; Conserv

Best Loca Matches

Query Match

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Misc-difference 44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is joined to the C-terminus of an N-terminal transcur. comprising opt. modified 'endamistate. This fusion protein may be converted into human insulin using known methods. The synthetic gene was prepared by the phosphoramidite method. See also AAOQ4336.

(Updated on 25-MAR-2003 to correct PR field.)
(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                     /label-Lys residue linking insulin B chain to A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPI; glycosylphophalidylinositol; insulin: hormone; solubilitation;
Saccharomyces cerevisiae; anchor; Gasl; plasmid phy40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHILLFORD STANDARD S
                                                                                                   Proinsulin analogue with a Lys residue linking the A and E chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New insulin fusion proteins comprise pro-insulin analogue linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosylphosphatidylinositol-anchored human recombinant insulin.
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Live 2; Mismatches 0; Indeis
                                                                                                                                            insulin fusion protein; pro-insulin analogue; tendamistate;
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                                                                                                                                                                                                                                                                                                               Ziabel Insulin B chain 37,.57
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/label- Insulin A chain
                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure: Page 2: 2pp: Serman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88DE-3837273.
89DE-3927443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89EP-0120056
                                        (updated)
(first entry)
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(first entry)
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Best Local Similarity 96.2*
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 1996 141149/19.
N-PSDB: AAQ04335.
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                                                                                                                                                                                                                                                                  misc-difference
                                                                                                                                                                 Lys-Lys bridge;
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19-AUG-1989;
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                                        25-MAR-2003
14-SEP-1990
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24-JAN-1996
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                                                                                                                                                                                                       synthetic
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AAR64582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant produ. of proteins, e.g. insulin - by producing the protein with a glycosyliphosphatidylinositol anchor followed by selective release.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.1%; Score 288.5; DB 16; Length 160; ilarity 98.1%; Pred. No. 6.1e-17; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                               Amaral De Castilho Valavicius
                                                                                                          (ESCO-) ESCOLA PAULISTA MEDICINA.
(FINE-) FINEP FINANCIADORA ESTUDOS & PROJETOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 16, 2003, 12:38:26 Job Line : 33.642 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 3; 51pp; English.
95WO-BR0001C
                                                        94BR-0000600
                                                                                                                                                                                            Cardoso De Almeida Mi,
Gomes De Amorim Filho A;
                                                                                                                                                                                                                                                                            WPI; 1995-302726/39.
N-PSDB: AAQ99460.
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nes 53; Conserv
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                                                        7-FEB-1994;
16-FEB-1995;
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Gendare Version 5000 Copyright (c) 1994 - 2003 Chemagen Lid
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using sw model - protein search, OM protein September 16, 2003, 12:37:10 p. Seerch task 17:37 Seconds (Without alignments) 255,217 Million cell updates/see Run on:

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US-09-423-100-6 587

1 MPPTIPLSRUFDNAMLRAHR... Title: Perfect score: Sequence: BICSUM62 Gapop 10.0 , Gaphixt 0.5 Scoring table:

328717 seqs, 42310858 residues Searched: Total number of hits satistying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 03 Maximum Match 1608 Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodate/1/iaa/5A_CCMB.pcp:*
2: /cgn2_6/ptodate/1/iaa/55_COMB.pcp:*
3: /cgn2_6/ptodate/1/iaa/5A_COMB.pcp:*
4: /cgn2_6/ptodate/1/iaa/5B_COMB.pcp:*
5: /cgn2_6/ptodate/1/iaa/PCTUS_COMB.pcp:*
6: /cgn2_6/ptodate/1/iaa/PCTUS_COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equa, to the score of the result being printed, and is derived by analysis of the total score distribution.

SCHWARIES

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Result No.	Score	Overy Match	Duery Match Length	62	g:	nestration (perion
, ,	304	51.8	9		CS-08-160-376A-6	Sequence 6, April
7	302.5	51.5	137		US-08-460-256-39	5
æ	302.5	51.5	137	·*·.	68-08-975-365-39	Sequence 19. App
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u)	239	90.9	95	-		r.
φ.	599	50.9	3.5	-	US 08-389-487 11	
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5	299	50.9	145	1	38-08-430-256-45	Sequence 45. App
10	299	50.9	145	~	US-08-975-465-45	4
11	299	50.9	246	_	US-08-400-256-48	r.
12	299	50.9	957	~	08-08-975-365-48	(1) **
13	293	49.9	57	٠.	US-06-030-731A-44	Sequence 45. An
14	287	48.9	65	~	US+08-900-574-3	Sequence A. Apr.
15	286.5	8.8	99	~.	08-08-900-574-5	u'
16	286	48.7	67	m	US 08-900-574 7	ľ
1.7	264.5	48.5	53	-	US-08-468-674B-71	
60 F 1	284.5	5.8	65	~	US-98-780-571-71	Sequence II. April
19	284.5	48.5	124	۲,	US-03-012-669F-36	
20	284	च . इ.स.	138	~	US-08-932-082-19	Sequence 19. Apr
21	284	₹. 82 •	140	~	US-08-400 (256-33	Sequence 41. Apr
22	284	T. 60	140		US-58-400-256-42	Sequence 42. Apr
23	294	48.4	140	~	JS-08-975-365-33	•
24	284	4.8.4	140	~	US-08-975-365-42	4
25	283.5	48.3	53	-	US-08-233-617-4	
56	283.5	48.3	53	4	US-C8-981-988A-42	(N
27	283.5	48.3	1117	~	US-09-012-669F-37	ند) در

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Gaps

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53.8%; Score 304; DB 1; Length 63; 94.7%; Pred. No. 7.3e-29; tive 0; Mismatches 3; Indels

Query Match Best Local Similarity 94.7 Matches 54, Conservative

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US:08-400-256-15	US-08-975-365-15	JS-08-468-674B-41	US-08-780-571-41	US-08-468-674B-45	US-08-780-571-45	US-28-446-546-3	US-07-918-953-8	US-68-081-661-8	38-69-477-92 4 -3	US-09-723-981-3	JS-09-723-896-3	US-08-280-030-63	US-08-233-617-3	US-09-134-836-4	US-09-386-303A-4	US-08-160-376A-4	US-08-400-256-36
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281	282	S. S. S.	280.5	280.5	280.5	280.5	279.5	279.5	278.5	278.5	278.5	278	277.5	277	277	277	277
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ALIGNMENTS

APPLICANT: Obermeier, Ranier
APPLICANT: Gerl, Martin
APPLICANT: Gerl, Martin
APPLICANT: Lidwig, Jurgen
IITLE OF INVENTION: Process For Obtaining Proinsulin
IITLE OF INVENTION: Possessing Correctly Linked
IITLE OF INVENTION: Cystine Bridges
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: Kenneth A. Genoul, Esq.
STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500 DISKETTE, 3.5 INCH, 1.44 Mb STORAGE FILING JATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: BATBAIA V. MATTER; ESQ.
REFERRATION NUMBER: 31,287
REFERRENCE/COCKET NUMBER: 40E 92/F 384
TELECOMMUNICATION: INFORMATION: OPERATING SYSTEM: WINDOWS 3.1 SORTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/160,376A ; Sequence 6, Application US/08160376A; Patent No. 5473049 TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACIERISTICS: 63 Amine Acids not relevant TYPE: Amino Acid (AA) New Jersey : U.S.A. GENERAL INFORMATION: CCUNTRY: U US-28-163-576A-6 08-08-160-376A-6 TOPOLOGY STATE: RESUL: 1

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Washington
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                                                                                                                                                          STATE: New York
                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, for
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPTIPLSRLFDNAMERAHGLAFOTYQEFEBAYIPKEC KYSFLQ------N 48
GTGPRPVNQHLCGSHIVEALYIVCGSRGFFYTFKTRGIVPDCCTSIOSIYQLENYCN (6)
                      DB 1: Length 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0. Version #1.25 CURRENT APPLICATION NATA: PAPLICATION NAFA: US/06/400.256 FILMS DAIR: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 51.5%; Score 302.5; DR L; Best Local Similarity 50.0%; Pred. No. 2.9e-28; Matches 76; Conservative 4; Mismatches 27;
                                                                                                                                                                                         APPLICANT Havelund, Svend
APPLICANT Halstrom, John
APPLICANT JORGESSON, 16
APPLICANT Anderson, Asser Sloth
APPLICANT MAKEUSSON, 13
APPLICANT ACVLATED INSULIN
NUMBER OF INVENTION: ACVLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE AUDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3985.220-08
                                                                                                                                                                                                                                                                                                                                                                                                          New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONDUTER HEADABLE FORM:
MEDIJM TYPE: Floppy disk
COMPUTER: IRM PC COMPATILLE
OPERATING SYSTEM: PC-07/82/MS-IDS
                                                                                            RESULT 2
US-08-400-226-39
Sequence 39. Application US/08460256
Patent No. 5750497
GENERAL INFORMATION:
APPLICANT: Havelund, Svend
: APPLICANT: Havelund,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
APPLICANT: Havolund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/ASENT INFORMATION:
NAME: Lumbirs, Ellas J.
REGISTRATION NUMBER: 53,728
REFERENCE/COCKET NOMBER: 3988.
TELECOMMONICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-878-3655
INFORMATION FOR SEC 1D NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-400-256-39
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ZIP: 10:74-6401
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US-08-975-365-39
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E: No. 60110070 No. 6011007disk of No. 6011007th America, Inc. 405 Lexington Avenue, 64th Floor
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GENERAL INFORMATION:
APPLICANT: Dorschug, Michael
APPLICANT: Moller, Klauds-Peter
APPLICANT: Marquart, Rudiger
APPLICANT: Meiwes, Johannes
TITLE OF INVENTION: An Enzymatic Process for the
TITLE OF INVENTION: Conversion of Preproinsulins Into Insulins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: ADDRESS: 5
ADDRESSEE: Finnegan, Honderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                          SCFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: 08/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Overy Match 51.5%; Score 302.5; DB 3; Best Local Similarity 50.0%; Prod. No. 2.9e-28; Matches 70; Conservative 4; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NOBER: CS 36/460,256
FILING DATE: 03-NAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambirs, Elida J.
RECISTRATION NUMBER: 33,728
RECERENCE/DOCKET NUMBER: 3985.229-US
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            RY: United States of America
10174-6401
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAIING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 IVEQCCTSICSLYCLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-867-0123
TELEFAX: 212-678-9655
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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Washington
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Hest Local Similarity
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                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-389-487-11
                                                                                                                         7.5 - 08 - 160 - 376A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 299.5; DH 1; Length 66;
Pred. No. 2.6e-26;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ludwig, Jurgen
APPLICANT: Sabet, Walter
TITLE OF INVENTION: Process For Obtaining Profession:
TITLE OF INVENTION: Possessing Correctly Linked
TITLE OF INVENTION: Cystin: Bridges
CORRESPONDENCE: 7
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.44 Mt STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Kenneth A. Geloni, Esg.
F: Rt. 262-206 No. 3473049th/P.C. Box 2500
Somerville
ZIP: 2008-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: law to compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.44
CURRENT APPLICATION DATA:
                                                                                                                                                                                               ATTORNEY/AGENT INSCRANICE:
NAME: Elandi, Carol P.
REGISTRATION NIKBER: 32.26
REFERENCE/FOCKEI NUMBER: 62481.1165-02006
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELEFAM: (202) 408-4406
INFORMATION FOR ESO ID NO: 5:
LENGTH: 66 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/03/160.376A
FILING DATE: December 1, 1993
CLASSIFICATION: 530
                                                                                                                                          APPLICATION NUMBER: US/03/251,060B
FILING DATE: 08:AUG-1994
CLASSIFICATION: 435
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ZIP: CR876-1258
COMPUTER READABLE FCHM:
MEDLUM TYPE: DISKETTE: 3.5 INCH.
COMPUTER: ISM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 7, Application US/08150376A Patent No. 5473049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Barbara V. Maurer, Esq.
REGISTRATION NUMBER: 31,287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P
FILING DATE: December 2,
ATIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                      ) TOPCLGGY: linear
) MOLECULE TYPE: peptide
US-08-291-0608-5
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
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US-09-160-376A-7
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1 Similarity 100.0%; Pred. No. 2.46-28;
53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11. Application US/38389467
Patent No. 5663591
SENERAL INFORMATION:
SENERAL INFORMATION:
APPLICANT: Obermeter, Rainer
APPLICANT: Ludwig, Jureon
APPLICANT: Ludwig, Jureon
APPLICANT: Sabel, Walter
TILLE OF INVENTION: Correctly Linked Cystine Bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inders
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunor
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDICAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-506X/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NOMBER: 02481.1424-00600
TELECCMMUN:CATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cubry Match 50.9%; Score 299; DB Bost Local Similarity 106.0%; Pred. No. 2.4 Matches 53; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/389,487 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY AGENT: INFORMATION:
NAME: Elbaudi, Carol P.
EGISTRATION NUMBER: 32,220
TELEPHONE: (908) 231-4079
TELEARY: (968) 231-2255
INFORMATION FOR SEC ID NO. 7:
SEQUENCE CHARACTERISTICS:
LEWITH: SE Amino Acids
TYPE: Amino Acids
TYPE: Amino Acids
TELECLORY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 56 amino acids
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STRANDEDNESS:
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APPLICANT: Ger., Martin
APPLICANT: Ludwig, Jurgen
APPLICANT: Ludwig, Jurgen
TITLE OF INVENTION: Process for Obtaining Insuin: Having
TITLE OF INVENTION: Correctly Linked Cystine Bridges
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 96;
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                                                                                                                                                Process For Obtaining Proinsalin
Possessing Correctly Licked
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                                                                                                                                                                                                                                                                                                                                                                                                       DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                  ADDRESSEE: Kenneth A. Genoni, Esq. STREET: Rt. 202-206 No. 5473649th/P.C. Box 2500 CITY: Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 50.9%; Score 299; LPF 1: 3
Best Local Similarity 100.0%; Pred. No. 4.80-28;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Barbara V. Maurez, Esq.
REGISTRATION UNDHER: 31,287
REFERENCE/DOCKET NUMBER: 40E 92/F 384
TELECOMMUNICATION INFORMATION:
                                                   APPLICANT: Obermetor, Ramiter
APPLICANT: Gerl, Martin
APPLICANT: Sabel, Walter
TITLE OF INVENTION: Process For Obtain
TITLE OF INVENTION: Process For Obtain
TITLE OF INVENTION: Cysting Bridges
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Remeth A. Genopi, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: WINDOWS 3.:
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/160,375A
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// Sequence 5, Application US/U818.376A
// Patent No. 5473049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/083f9487
Patent No. 5663291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Dunner
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (908) 231-4076
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 96 Aniho Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: December
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  STATE: New Jersey COUNTRY: U.S.A. ZIP: 08876-1258
                                                                                                                                                                                                                                                                                                                                                                                                                             :BM 386
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CITY: Washington
STATE: D.C.
                                     GENERAL INFORMATION:
APPLICANT: Obermed
APPLICANT: Gerl, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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Patent No. 5750497
SEREAL INFORMATION:
SPETRAL INFORMATION:
APPLICANT: Halstrom, 3chn
APPLICANT: Gorassen, 1b
APPLICANT: Asser Sloth
APPLICANT: AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDA
COMPATER: IBM PC COMPALIDA
OPERATING SYSTEM: PC-DGS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/400,256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
CCMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMBUTER: IBM PC compatible
COPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Refease #1.0, Version #1.25
CURENT: APPLICATION DATA:
APPLICATION NUMBER: US/08/389,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62481.1424-00000
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COUNTRY: United States of America
21P: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Finaudi, Carol F.
REGISTRATION NUMBER: 32,20
REERRENCE/DOCKET NUMBER: 02481
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4460
INFORMATION FOR SED IS NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTOKNEY/AGENT INFORMATION:
NAME: Lambirs, Elias J.
REGISTRATION NUMBER: 33,726
REFERENCE/POCKET NUMBER: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MCLECUSE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21P: 10174-6401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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STATE: Nov.
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-975-365-48
                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                  55 REVNOHLGGSHIJARAZITAVGGERGFEYTEKTRGIJEBGGTTSTGSGZYGLBNYGN 147
1141 111-41141 111-41141 111-41141 111-4141 1111 1
93 REVNOHLGGSHIJARAZITAVGGERGFFYTEKTRGIZERGGTTSTGSTGSTGSTAFGRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 REVNOULCESHIVEALYLVCGERCFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                               ÷
                                                                                                 56.99; Score 299; DB 1; Legath 145;
100.38; Pred, No. 7.96-24;
Live C; Mismatches C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.9%; Score 299; DR 3; Londth 145; Best Local Similarity 120.0%; Pred. No. 7.36-26; Matches 53; Conservative C; Mismatches C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TORNEYAGGA, .... Flias J.
NAME: Lambiris, Slias J.
REGISTRATION NUMBER: 33.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: United States of America
ZIP: 1744-6401
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HR PC Compatible
COMPUTER: HR PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1945
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
APPLICANT: Have.und, Svend
APPLICANT: Halstrom, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-400-256-48
: Sequence 48, Application US/08400256
: Patent No. 5750497
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INFORMATION FOR SEQ ID NO: 45:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 145 amino acids IYPE: amino acid
                                                                                Ouery Match
Best Local Similarity 100.5
The S3: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                  MCLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Jonassen,
amino acid
                 linear
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                   TOPOLOGY:
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APPLICANT:
                                                          115-08-400-256-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 REVNOHLOGSHLVEALZLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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SOFTWARE: Patentin Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h Sone 299; DB 1;
Similarity 100.0%; Pred. No. 8e-28;
53; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3985.220-US
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APPLICANT: Johnsson, 1b
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
IITLE OF INVENTION: ACYLATED INSULIN
                                                                                         APPLICANT: MATKUSSEN, JAN
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                IX: United States of America
10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APFLICATION NUMBER: US/C8/400,256
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48. Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
APPLICANT: HAVELING, John
APPLICANT: Halstrom, John
                                           Jonassen, Ib
Andersen, Asser Sloth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEGESTHATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 398
REJECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-5123
TELEFAX: 212-876-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
Havelund, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATIORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 amino acids
                        Halstrom, John
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Σ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 130.
Matches 53, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : MOLECULE TYPE: protein
08-08-400-256-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                            New York
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STATE: New York
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PRIOR APPLICATION 514
PRIOR APPLICATION NUMBER: German Application No. 6221837 19630242.0
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Carol P. Eliandi.
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
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APPLICANT: Ert., Johann
APPLICANT: Habormann, Pau.)
APPLICANT: Geisen, Karl
APPLICANT: Selpek, Gerhard
TITLE CF INVENTION: Insulin derivatives with increased zinc
TITLE OF INVENTION: hinding
CORRESPONDENCE: 18
CORRESPONDENCE: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cory Match 45.9%; Score 293; DB 1; Length 57; Best Local Similarity 96.2%; Pred. No. 1.3e-27; Matches 51; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: LBM PC compatible
CDESATING SYSTEM: PC-TOSYMS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,574
FILING DATE: July 24, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Finnegan, Henderson, Farabow, Garrett,
: s Dunner, L.L.P.
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1499-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02481-0593-02000
                                                            APPLICATION NUMBER: DE P 38 37 273.8
FILING DATE: 03.NOV-1988
PRIOR APPLICATION DATA:
FILING DATE: 19-AUG-1989
RIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 39 27 449.7
FILING DATE: 19-AUG-1989
APPLICATION NUMBER: DE P 40 12 818.0
ATTORNEY/AGENT INFORMATION:
NAME: KITSCHNEY MICHACL K.
REGISTRATION NUMBER: 34.85;
REGERENCE/DOCKET NUMBER: 02481-0593-0201
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Segrence 3, Application US/08900574 Patent No. 6221837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: District of Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELLEPHONE: 202-408-4000
TELEFAX: 202-406-4400
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : (202) 408-4000
(202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 57 amine acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20005-3315
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ADDRESSEE:
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APPLICANT: Koiser, Klaus-Peter
APPLICANT: Koiser, Guenther Johannes
APPLICANT: Chimann, Bugen
TITLE OF INVENTION: Processes for the Preparation of Foreign
TITLE OF INVENTION: Protects for the Preparation of Foreign
TITLE OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.9%; Score 299; DH 3; Length 145;
100.0%; Pred, No. Re-28;
Live 6; Mismatches 0; Indols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCKTRY: USA
ZIP: 20005-3315
COMPUTER: REDABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIN:
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE P 37 14 866.4
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FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOV-1989
PRIOR APPLICATION NUMBER: US 07/587,610
FILING DATE: 19-APR-1391
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,757
APPLICATION NUMBER: US 07/735,757
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PRIOR APPLICATION DATA:
PRELICATION NUMBER
PILIMO TO NUMBER
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FILING DATE: 03-MAR-1995
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08(30731A Patent No. 5426036 GENERAL INFORMATION:
                                                                                                                                                                                                                                         NAME: Lambiris, Ellas J.
REGISTRATION NÜMBER: 33.728
REFERENCE/DOCKET NUMBER: 3985
TELECOMMUNICATION INFORMATION:
TELEFAN: 212.867.0123
TELEFAX: 212.867.0123
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 146 amino acids
amino acid
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Best Local Similarity 160.6
Matches 53, Cosservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 0
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                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application 35/6860574
Patent No. 6221837
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Erly, Johann
APPLICANT: Gelsen, Karl
APPLICANT: Gelsen, Karl
APPLICANT: Seipke, Gernard
TITLE OF INVENTION: Insulin derivatives with increased zinc
MUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         48.9%; Score 262; PR 2; Evagah 65: 91.4%; Pred. No. 7.70°.27; 515 5170°.00 Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett,
ADDRESSEE: & Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Carol P. Einaudi
RECISTRATION NUMBER: 32,129
REFERENCE/DOCKET NUMBER: 02481.1499-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 35/38/300.574
FILING DATE: 3uly 24, 1937
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NORMER: German Applicat
FILING DATE: dity 26, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: District of Columbia COUNTRY: U.S.A. Z.P. 20005-3315 COMPUTER REACABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: Protein
CRISIMAL SCURCE:
ORGANISM: Escherichia rol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia cott
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(202) 408-4400
NR SEG ID NO: 5:
                                                65 amino acids
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INFORMATION FOR SEQ ID NO:
                       SEQUENCE CHARACTERISTICS:
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LENGTH: 66 aming c...
TYPE: Action acid
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ORIGINAL SOURCE:
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Best Local Similarity
Matches 53; Conserva
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                                                                  Amine acid
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TYPE: Amino ac
STRANDEDNESS:
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US-08-900-574-3
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US-08-900-574-5
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472.415 Million rell appartes/sec
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Genlore version 5.1.5
Copyright (c) 1993 - 2003 Compuger Edd.
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Listing first 45 summaries
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Maximum DB seg length: 2600000000
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587
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Perfect score:
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                                                                                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result beam princed and is derived by adalysis of the total score distribution.

SUMMARLES

Pescrip: to:	Sequence 6, App. 1		Sequence 8, Apr	<u>.</u>	Sequence 15, Art	Sequence 7. Apply	Sectionary April	Sequence 63, Apr.	Control of schools	Sequence 12, April	Sequence 12, April			Sequence 16, App.	Sequence 10, Appl
110	US-10-054-873-6	US-10-054-873-7	US-10-654-873-5	US-06-864-711-1H	US-69-861-687-19	08-09-858-6358-5	US-10-028-410-3	US-09-280-030-63	US-09-947-563-4		US-09-740-359-12		US-09-736-611-10	US-09-740-359-10	US-09-894-711-10
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Length	107	150	55	124	3.38	ųñ.	5.		36	124	124	124	12	1.25	1.25
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Score	5.87	555.5	294	284.5	284	278.5	278.5	278	277	275.5	275.5	275.5	275.5	275.5	275.5
Resul: No.	-1	?	9	•	v	9	į.	80	6	10	11	12	13	14	15

Sequence 8, Appli Sequence 7, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli	VO.	Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 175, Appli	Sequence 3, Appli Sequence 9, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli	Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 23, Appli Sequence 1, Appli	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli	Sequence 66, Appl. Sequence 7, Appli. Sequence 2, Appli.
US-09-736-611-8 US-09-740-359-7 US-09-736-611-6 US-09-740-359-5 US-09-894-711-5				US-10-328-813-2 CS-10-054-873-1 US-10-054-873-2 US-09-984-010-23 US-10-153-207-1		US-09-280-030-56 US-09-894-711-7 US-09-853-688-2
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AL I GNMENTS

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RESULT:

US-10-054-873-6
US-10-054-873-6
Sequence 6, Application US/10054873
Publication No. US20020;647124
GENERAL INFORMATION: Chimeric Protein Containing an TIILE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 8 PRACTISES
ADDRESSEE: Townsond and Townsond and Crew LLP STREET: Two Embarcadero Center, Eighth Floor STRIE: California COUNTRY: USA
COUNTRY: USA
COMPUTER: HBM PC COMPUTER: BUS 44111383
COMPUTER: BAD COMPUTER: BUS COMPUTER: BUS 45110 NOT COMPUTER: BUS BOUNDER: BUS EQUENCE CHARACTERISTICS:
BUS COMPUTER: BUS COMP
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6) TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLGGSHLVEALYLVGGER 120
                                        FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 69/423,100
FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEG ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/894,711; CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORK:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kjeldsen, Thomas Borglum APPLICANT: Ludvigsen, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 18, Application US/09894711
Patent No. US20020137144A1
                                                                                                                                                                                    Sequence 5, Application US/10054873
Publication No. US20020164712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STAIE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Bost Local Similarity 100.0
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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IIIIE CF INVENTION: Chineric Protein Containing an
Intramolecular Chaptron-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.6%; Score 555.5; DB 14; Length 150;
llarity 71.3%; Pred. No. 5e-59;
Conservative 0; Mismatches 0; Indels 43;
                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                       61 LOGSHLVEALYINGGERGFFYTPKTRGIVEQCCTSICSLYQLENYON 107
                                                                                                                                                                                                                                                                                                            indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPERATING SYSTEM: ECLOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/15/054,#71
F1LING DATE: 22-Jar -2002
CLASSIFICATION: JGH KNOWHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsen, and Crow Lip
STREMT: Two Embarcadero Center, Elabith Floor
CITY: San Prancisco
STATE: California
                                                                                                                        100.0%; Score 587; DB 14;
100.0%; Pred. No. 5.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 020167-00013008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WC PCT/CN98/00052
FILING DATE: 31-MAE-1999
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEG ID NG: 7:
                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-1834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10054873 Publication No. US20020164712A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 150 amino acids TYPE: amino acid
STRANDEDNESS: <Unkrown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACIERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                      Ouery Match
Best Local Similarity 100.0
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             US-10-054-873-7
                                                                               US-10-054-873-6
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APPICANT: Ludvigsen, Svend
TITLE OF INVENTION: Method for making insulin precursors and
TITLE OF INVENTION: insulin precursor analogues having improved fermentation
TITLE OF INVENTION: yield in yeast
FILE REFERENCE: 6148,400-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | FVNQFLCGSH;WFALVLVGGERGFFTTPKIRGIVEQCCTSICS;YQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
O
                                                                   Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANI: Gan, Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: IOWNSEND and COMPANIAN STREET: Two Fmbarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/POCKET NUMBER: 020167-090130US
:NEORMATION FOR SEO ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.1%; Score 294; DB 14;
100.0%; Pred. No. 4.1e-28;
17vc 0: Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHIOR APPLICATION DATA: APPLICATION NUMBER: WO PCT/CN98/00052
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                                                                                                                                                                                                                                                                                                                                                 2 FPTIPLSRLFDNAMLRAHRLHOLAFDTYOEFEEAYIPKEO--KYSFLQ------N 48
                                                                                                                                                                                                                                                                                                                                                                                                                   3 FPSI----FTAVLFAASSALAAPVNTITEDETAQIPAEAVIGYSDLEGDFDVAVLPFSN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 PLGTG - - - - - - - - - - - - - - - PREVNOHLCGSHLVEALYLVCGERGFFYTPK - TR 86
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Deboquie, Yves
APPLICANT: Plavaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
TITZ OF INVENTION: MEHOD FOR TREATING CARTILAGE DISORDERS
FILE REPERCOE: P194R1
CURRENT APPLICATION NUMBER: US/09/868,9358
CURRENT FILMG DATE: 2002-07-02
PRIOR FILMG DATE: 2006-11-15
PRIOR FILMG DATE: 2006-11-15
PRIOR FILMG DATE: 2006-05-16
PRIOR FILMG DATE: 2006-05-16
NUMBER: OF SEQ ID NOS: 153
LENGTH: 51
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                                                                                                                                                                                              Score 284; DB 10; Length 138; Pred. No. 2.2e-26;
                                                                                                                                                                                                                                                                       28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adels
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                                                                                                                                                                                                                                                                       5; Mismatches
                                      MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: CS/10/028,410
CURRENT FILING DATE: 2001-12-19
PRICE APPLICATION NUMBER: 35/69/477,924
FRICE FILING DATE: 2000-01-35
FRICE FILING DATE: 2000-01-35
SEQ ID NO 3
JENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 GIVEQCCISICSLYQLENYCN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 GIVEQCCTSTCSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09858935B Publication No. US20330069177A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application CS/10028410 Publication No. US20020166955A1 GENERAL INFORMATION:
                                                                                                                                                                                          Owery Match
Sest Local Similarity 48.28;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dubaquie, Yves
APPLICANT: Lowman, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-858-935B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ORGANISM: Homo sapiens
US-10-028-410-3
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Matches 51; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CS-08-828-335B-5
                                                                                                                    US-09-861-687-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRI
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STREDI: 405 Dexington Avenue, 54th Floor
CITY: Now York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 PREVNQHLCGSHLVEALYLVGGERGFFYTPK-IRGIVEQCCISICSLYGLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: [HILL] HELL: HILL: HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 48.5%; Score 284.5; DB 10; Dength 124: Best Local Sinitarity 92.7%; Prod. No. 1.76-26; Matches 51; Conservative 2; Mismatches 1; Lidels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READANTE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FO COMPUTED!
OPERATING SYSTEM: PC-DOS/MS-LCS
SOFTWARE: Patontic Neleaso #1.5, Vorsion #1.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 4341.204-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brandt, Jakob
Kurtuhais, Peter
Hansen, Hertz Per
Kaarsboim, Niels Christian
INVENTION: INSULIN DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America 2:P: 10174-6401
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                       PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: PA 1999-61869
PRIOR FILING DATE: 1999-2-2-23
PRIOR PELICATION NUMBER: 60/211.031
PRIOR FILING DATE: 2000-66-13
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 68/932,082
FILING DATE: 16-DEC-1997
PRIOR APPLICATION NUMBER: PA 2000 00443
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REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-May-2001
CLASSIFICATION: <UCKNOWE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-861-687-19
Sequence 19, Application US/09861687
Publication No. US2002019329281
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-867-0123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Markussen, Jan
Jonassen, 15
Havelund, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-878-9655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic US-09-894-711-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: INSINUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CARACTOR Thomas
APPLICANT: Lodvigser, Svend
APPLICANT: Lodvigser, Svend
APPLICANT: Lodvigser, Svend
APPLICANT: Karsholm, Niels
TITLE OF INVENTION: Method For Making Insulin Precursors and
TITLE OF INVENTION: Insulin Precursor Analogs
FILE REFERENCE: 6056.200-05
CURRENT APPLICATION NUMBER: CS/09/736.611
PRIOR APPLICATION MIMBER: 60/181,443
PRIOR FILING DATE: 2000-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 96;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/05/947,563
FILING DATE: 07-569-2001
CLASSIFICATION NUMBER: US/05/947,563
FILING DATE: 07-569-2001
CLASSIFICATION DATA:
APPLICATION WINDER: 09/134,836
FILING DATE: clorknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDonal 34,872
REFERENCE/COCKET NUMBER: 02481.1600-000C0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (08-4400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.2%; Score 277; DB 10; Best Local Similarity 59.3%; Pred. No. 9.8e-26; Matches 54; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GIGPRFVNQHLCGSHLVEALYLVCGERGFFYIPKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 -----RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 LALEGSIQKRGIVSQCCTSICSLYQLENYCN 96
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PRIOR APPLICATION NUMBER: 60/211,441
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 1000-06-13
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEO ID NOS: 18
SOFIWARE: FASTSEO for Windows Version 4.0
SEO ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-736-611-12

Sequence 12, Application US/09736611

Patent No. 0820016023059A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 10 No: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIRANDEDNESS: single
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ORGANISM: N-terminal extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-736-61:-12
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TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded eystine bridges
                                                                                                               --
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 63, Application US/09280030A
PRICAL INFORMATION:
APPLICANT: Sato, Seij
APPLICANT: Kondo, Toshiyuk!
APPLICANT: Nondo, Masaaki
APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Designated is OTHER INFORMATION: an amino acid sequence of OTHER INFORMATION: MWPsp-MWPmplD-Mot-Pro:nsulin
                                                                                                                                                                         56 FVNQHLGGSHLVEALYLVGGRGFFYTPKTRGTVBQCGTSTGSLYGLENYCN 107
                                                                                                                                                                                                                    _
                              Query Match 47.4%; Score 278.5; DB 14: Longto 51: Best Local Similarity 98.1%; Pred. No. 2.96-26; Matches 51; Conservative 0: Mismatches 0: Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
47.44, Score 278, 18 3; Length 117,
Best Local Similarity 60.38; Pred. No. 9.5e-25;
Matches 54; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 TGPREVNQHIGGSHLVEALYLVCGERGFFY;FKT ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 -----RGIVEQCOTSICSLYQLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 382.1226
CURRENT APPLICATION NUMBER: US/09/280.03CA
CURRENT FILING DATE: 1999-35-26
EARLIER APPLICATION NUMBER: JP10-87339/1998
BARLIER FILING DATE: 1998-33-31
NUMBER OF SEO 10 NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 26005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rubroder, Franz-Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1300 I Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGIH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-280-030-63
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GENERAL INFORMATIONS
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SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-09-746-611-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Demas Borqlum
APPLICANT: Lidvigsen, Svend
TTLE OF INVENTION: Method for making insulin precursors and
TTLE OF INVENTION: Method for making insulin precursors and
TTLE OF INVENTION: Method for making insulin precursors and
TTLE OF INVENTION: yield in yeast
FILE REFERENCE: 614e1200-US
CURRENT APPLICATION WIMERE: PA 2000-0443
PRIOR APPLICATION WIMERE: PA 2000-0643
PRIOR FILING DATE: 2000-09-17
PRIOR PLING DATE: 1999-12-29
PRIOR PLING DATE: 1999-12-29
PRIOR PLING DATE: 2000-06-13
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEU ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-694-711-12
Sequence 12, Application US/09894711
Sequence 12, Application US/09894711
Sequence 12, Application US/09894711
Sequence 12, Sequence 12, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 14, Sequence 17, Sequence 1
                                                                                                                                            Simple : Simple
                                                                                                                                                                                                                                                       54 PREVNQHLOSHI VBALXI VOCERGPTIFKT ROLYBOOTTSICSEFULLATION 147 (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (11.1.11) (1
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46.9%; Score 275.5; DB 3; Length 124;
Best Local Similarity 90.9%; Pred. No. 2.1e-25;
Matches 56; Conservative 2; Mismatches 2; Lidels 1
Tength 1240
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US-09-746-359-12
46.9%; Score 275.5; DB 9;
90.9%; Pred, No. 2.16-25;
ive 2; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ 15 NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 1D NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Sequence 12, Application US/09740359
. Patent No. US20010041787A1
                                                                                                                                     50; Conservative
Query Match
Hest Local Surilarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                               Matches
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Squence 16, Application US/09740359

Squence 16, Application US/09740359

Squence 16, Application US/09740359

Squence 16, Application US/09740359

Squence 10, US/001004178741

Special Information: Information: Applicant Eddingsen, Swend

STITE OF INVENTION: Method for maxing insulin precursors and STITE OF INVENTION: insulin precursor analogues having improved fermentation: STITE OF INVENTION: MABER: US/09/740.359

CURRENT APPLICATION NUMBER: US/09/740.359

CURRENT PILING DATE: 2000-03-17

PRIOR FILING DAIE: 2600-03-17

PRIOR FILING DATE: 2900-06-13

PRIOR FILING DATE: 2000-06-13
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APELICANT: Ludyisen, Svend
TILLE COF INVENTION: Method For Making Insulin Precursors and
TILLE COF INVENTION: Insulin Precursor Analogs
FILLE REPERENCE: 6058-2004 Sy/09/736,611
CURRENT PAPLICATION NUMBER: 35/09/736,611
PRIOR APELICATION NUMBER: 60/181,443
PRIOR PILING DATE: 2000-05-13
PRIOR APELICATION NUMBER: 60/211,441
PRIOR APELICATION NUMBER: PA 1999 01868
PRIOR PILING DATE: 2000-06-13
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: DATE: PA 2000 00440
PRIOR FILING DATE: PA 2000-03-17
PRIOR FILING DATE: PA 2000-03-17
                                                                                                                                                                                                              ..
r 1
                                                                                                                                                      Score 275.5; DB 1G; Length 124;
Pred. No. 2.1e-25;
2; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuery Match 46.9%; Score 275.5; DB 9; Best Local Similarity 90.9%; Pred. No. 2.1e-25; Matches 50; Conservative 2: Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NOS: 18
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09736611
Patent No. US20010023069A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: N-terminal extension US-09-736-611-10
TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                         Ouery Match
Sest Local Similarity 90.9%;
Matches 50; Conservative
                                            FEATURE:
CTHEM INFORMATION: Syntheric
US-09-894-711-12
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Sequence 16, Application US/09894711
Patent No. US2020137144A1
GENERAL INTERNATION:
APPLICANT: Judyigsen, Svend
TITLE OF INVENTION: Method for making insulin precursors and
TITLE OF INVENTION: Method for making insulin precursors and
TITLE OF INVENTION: Method for making insulin precursors
TITLE OF INVENTION: 9'cld in yeas.
FILLE REPREDENCE: 6148 4400.45
FILLE REPREDENCE: 6148 4400.45
FILLE REPREDENCE: 6148 4400.45
FRIOR APPLICATION NUMBER: DA 1999 01859
PRIOR FILLING DATE: 2006-06-13
PRIOR FILLING DATE: 2006-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.9%; Score 275.5; PS 10; Longth 1259
Best Local Similarity 90.9%; Pred. No. 2.16-25;
Matches 50; Conservative 2; Mismatches 2; Indels 19
                                                                                                                                                                                                                                                                                                                                                 Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indeas
                                                                                                                                                                       EBNGTH: 125
TYPE: PKT
CRGANISM: TA39 leader fused with N-terminally extended
US-09-740-359-10
                                                                                                                                                                                                                                                                                                                                       Ouery Match 46.9%; Score 275.5; DB 9; Best Local Similarity 90.9%; Pred. No. 2.1e-25; Matches 50; Conservative 2; Mismatches 2;
                                                                          SEQ 1D NOS: 16
FastSEQ for Windows Version 4.0
   66/181/450
                               PRIOR FILING DATE: 2600-02-10
UNDBER OF SEQ 1D NOS: 16
SOFTWARE: FASTSEQ for Windows SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic
US-09-894-711-10
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-894-711-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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Search completed: September 16, 2003, 12:52:26 Job time : 34.7237 sers

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Gendore version 5.1.6 copyright (c) 1993 - 2003 Compages Ltd.
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OM protein - protein search, using sw model

September 16, 2003, 12:36:15; Search Ume 15:4903 seroids (Without allianments) 825:645 Million cell updatos/ser Rus on:

US-09-423-100-6 587 1 MEPTIPLSRLFDNAMLRAHRIVEGGGTSTGSLYGGENYGN 107 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 / Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Cisting first 45 summaries

Database :

PIR_76:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*				
Result		Ouery				
SO.	Score	Match	Match Length	90	10	pescription
П	275	46.8	96	~	PC7082	epidermal growth :
2	273.5	46.6	51	-1	LINWHE	
m	273.5	46.6	5.	ı-4	INWHE	Finback institution
₹.	273.5	46.5	51	٠.4	INEL	insulin - elephant
S	273	46.5	110	?	542179	ä
9	273	46.5	110	~	J00178	
۲۰	271.5	46.3	51	- 1	INHV	
æ	258.5	45.7	7.5	-	INMSSE	
σ	267.5	45.6	51	(4	A54151	institut orecursor
10	267	₹. 	110	-	TPHC	Ξ.
:1	267	45.5	110	:~)	A42179	Ξ
12	263.5	6.	15	۲.	INWHIS	2
13	263.5	6.4	51	٠.	INGI	
14	263.5	44.9	52	-	INCMA	insulto Arabian
1.5	263	44.8	84	~	IPPG	14. 21
16	263	3.44	0.1		HVRB	insuling production
17	262.5	44.7	5	_	CONT	the - minst
18	262	44.6	1:0	~	ZPDG	insulto preduce 2
61	261.5	44.5	5.1	_	LNAKKO	s nommac - niinsa;
20	260	44.3	116	~	148166	10.
21	258.5	44.0	105	-	IPBO	theory of the present
22	257	43.8	168	\sim	A39983	insulta promiser
23	256.5	43.7	5.	:N	700362	insuling North Am
24	255.5	43.5	217	-	STHC	socatorios: pre
25	255.5	43.5	217	?	167410	- Hido
56	252.5	43.0	77	r +	INSH	insulia produrson
27	252	42.9	85		IPHO	insulin precursor
28	251.5	42.8	51		INCH	insulin - Chinchil
59	250	42.6	108	r 1	INMST	insulin i rrecits:

insulin 1 precurso	insulin - goose	insulin 2 precurso	insulin 2 precurso	insulin 11 - North	insulin 12 - North	insulin precursor	insulia - crested	insulin - turkey (insulin - ostrich	insulin - black-be	insulin - slider t	insulin precursor	insulin - Amphiuma	insulin - duckbill	insulin precursor
IPRI	INGS	IPRT2	INMS2	S44469	S44470	151221	Odni	INTK	SONT	A61129	A66414	IPCH	561361	563590	IPDK
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210	 	110	:13	25	52	103	51	51	5.1	51	21	107	55	S	81
42.4	42.3	42.2	42.2	6.4	ور د د د	47	4	47.7	4	47	47	40.8	40.5	40.1	39.8
		m	ထ	ψ	ψ.	L'i	S.	vԴ.	w)	u)	'n,	ĸ)	е 20	ĸ.	ın.
249	248.5	246	24	24	2	?	244	244	244	244	244	239	?	255	233

ALIGNMENTS

Richersation PCORES, PCORE PCORE, Marchest Land PCORES, Excertion of Des-BSO Single-Chain Actives; Excertedhol PCORES, Excertion of Des-BSO Single-Chain Active For our bearings of the proper of the proper

Query Match

RESULT 3

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Affile: Sequences of primate insulin genes support the hypothesis of a slower rate ARE ference number: A42179; MCLD:92219953; PMID:1560757 AACCESSION: B42179
                                                                                                                                                                                                                                                                                                                    A.Cross-references: EMBL:X61092; NID:922808; PIDN:CAA43405.1; PID:922809
A.Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
K.Pererson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4866-4871, 1972
A.Title: Determination of the amino acid sequence of the monkey, sheep, and dog proi.
A.Reference number: A92111; MUID:72258016; PMID:4626369
A.Reference number: A92111; MUID:72258016; PMID:4626369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lisuils precursor - crab-cating macaque
Cospenies: Macaca fascicularis (crab-eating macaque)
Cospenies: Macaca fascicularis (crab-eating macaque)
Cospenies: Macaca fascicularis (crab-eating macaque)
Cospenies: Macacasion: J00178
P.Worokam, W.; Groneberg, J.: Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
Gene, 19, 179-183, 1982
A.Tille: The nucleotide sequence of cDNA coding for preproinsulin from the primate.
A.Rocession: J00178; MJJD:R3080474; PMID:6184262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 PAFVNOHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPØVGØVELGGGPGAGSLQPLAL 82
                                                  Species: Geroopitheous aethiops (green monkey, grivet)
Clate: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
Clacession: B42179; A60522; S16494; S22056
MKSeino, S.; Bell, G.I.: Li, W.H.
MGL: Biol. Evol. 9, 193-203, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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C.Suporfacily: Insulin
F:1-24/Pomain: signal sequence #status predicted <SIG>
F:25-54/Pomain: insulin chain #status predicted <ART>
F:25-54/Pomain: insulin connecting C peptide #status predicted <CPT>
F:55-94/Pomain: insulin connecting C peptide #status predicted <CPT>
F:90-110/Pomain: insulin chain # #status predicted <ACH>
F:31-96,43-109,95-100/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 PREVNQHLCGSHLVEALYLVCGERGFFYTPKT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F157-87/20main: connecting peptide *status experimental *96-110/Domain: insulin chain A *status predicted <ACH>F11-96,43-109,95-109/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:25-54/Domain: insulin chain B *status predicted <BCH>
F:25-54,90-110/Product: insulin *status predicted <MAT>
F:57-87/Jomain: connecting peptide *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Reywords: hormone; pancreas
F:1-24/Jomain: signal sequence *status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 273; DB 2;
Pred. No. 2.2e-21;
0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 -----RGIVECCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.58;
                              thatlin precursor - green monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.28
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.2
Matches 53: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Molecule type: protein
A)Residues: 57-87 <PET>
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Molecule type: mRNA
A:Residues: 1-110 <WET>
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-110 <SEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Introns: 63/1
C:Superfamily: insulin
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AsResidues: 1-30:31-51 <SM1>
AsNote: the species of elephant is not given, but it is sost probably the tuben elephan
                                                                                                                                                                                                                                                                                                                                                                                             CySpecies: Elephantidae gen. sp. (elephant)
Cybare: 24-Apr-1984 #sequence_fevision 30-Sep-1988 #lext_change 16-jul-1999
CyAncession: A01584
RySmith, E.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sdeb
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                                                                                                                                                                                                                     56 FVNQHIGGSHLVEALYEVGGERGFFYTPKTRGTVEGGGTSIGSLYGLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVNOHEGGSHLVEALVGSERGFFYTFRA-GIVEGYTS ISSLYGGENYCK ST
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                                                                                                             Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 51;
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                         F:31-51/Domain: insulin chain A *status experimental <ACH>
F:7-37,19-50,36-41/Dissifide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C)Superfamily: insulin
C)Kcywords: hormone; pancreas
F)1-30/Domain: insulin chain 5 *status experimental <BCH*</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Am. J. Med. 40, 662-565, 1965
Affile: Species variation in the amino acid sequence of
A/Reference number: A90029; MUID:66160119; PMID:5949593
A/Accession: A01584
Fil-30,31-51/Froduct: insulin #status experimental < MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UB 1;
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                                                                                                          Score 273.5; DB 1:
Pred, No. 8.7e-22;
): Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.6%; Score 273.5; DB 1 96.2%; Pred. No. 8.7e-22;
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                                                                                                             46.68;
96.28;
                                                                                                                                   Best Local Similarity 96.2
Matches 50, Conservative
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Matches 50; Conserv
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Query Match

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Query Match Matches

RESULT 5

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Riclivelra, A.B.A.; Machado, O.L.T.; Gomes, V.M.; Xavier-Noto, J.; Pereira, A.C.P.; Frotein Pept. Lett. 6, 15-21, 1999
Airitie Jack bean seed coat contains a protein with complete sequence homology to Airitie. Jack bean seed coat contains a protein with complete sequence homology to Aireference number: A59151
Airocession: B59151
Airocession: B59152
Airocession: B59153
Airocession: A59153
Airocession: A59153
Airocession: A59154
Airocession: A59154
Airocession: A59154
Airocession: A59155
Airocession: A59154
Airocession: A59155
Airocession: A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CiSpecies: Homo sapiens (man)
CiDate: 24-Oct.1981 *Sequence_revision 23-Oct.1981 #text_change 08-Dec-2000
CiAccession: A93222, A94253; A93216; A94251; A93144; A92075; A91186; IS8114; A01579
Pibeli: Gil: Pictor, R.L.; Rutter, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.
Nature 284, 26-32, 1980
             J.; Pereira, A.C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ
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H.M.; Rutter, W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:J00265; NID:q186429; PIDN:AAA59172.1; PID:g386828 R:Bell, G.I.; Swain, W.F.; Pictet, R.; Cordell, B.; Goodman, H.M.; Rutter, Nature 282, 525-527, 1979
A:Title: Vucleotide sequence of a cDNA clone encoding human preproinsulin. A:Roferacce number: A93226; MUID:80654779; PMID:503234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTILES Sequence of the human insulin gene.
A.Reference number: 493222; KulD:80120725; PMID:6243748
A.Accession: A93222
A.Molecule type: DNA
A.Rocioule type: DNA
A.Rocioule type: DNA
A.Rocioules: 1-110 < RELA
A.COSS-Peferences: GB:J00265; NID:9186429; PIDN:AAA59172.1; PID:9386828
R.Ullirch, A.: Dull, T.J.: Gray, A.; Brosius, J.; Sures, I.
Science 209-212-15, 1960
A.Tille: Genetic variation in the human insulin gene.
A.Reference number: A94253; MUID:80236313; PMID:6248962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Molecule type: mRNA
A:Residucs: 2.110 <REL2>
A:Cross-references: GB:Z00265; NID:9186429; PIDN:AAAS9172.1: PID:9386B28
A:Gries: 1.; Goeddel, D.V.; Gray, A.; Ullrich, A.
Science 208, 57-59, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GR:J00265; NID:g186429; PIDN:AAA59172.1; PID:g366828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 EVNOHLGGSHJVEALXIJVGGERGFFYTPKTRGIVEOCCTSIGSEYQLENYGN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Title: NucleoLide sequence of human preproinsulin complementary DNA A:Reference number: A94251; MUID:80147417; PMID:6927840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVNOHLGGSH:VEALYLVGBRGFFYTPKA-GIVEQCASVGS:YQLENYCN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: protein
A:Residues: 25-54:90-110 <NTO>
R:Oyer, P.E.: Cho, S.; Peterson, J.D.; Steiner, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.6%; Score 267.5; DB 2
92.3%; Pred. No. 3.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RENICC, D.S.E.W.: Smith, L.F.
Nature 187, 483-485, 1960
Affile: Amino-acid sequence of human insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unsulin precursor [validated] - human N.Alternate names: preproinsulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 92.3%;
has 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Reference number: A93144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Accession: A94253
A.Molecule type: DNA
A.Residues: 1-110 <ULI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: mRNA
A:Residues: 1-110 <SUR>
A:Cross-references: SB:J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Accession: A93144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Accession: A94251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Cispecies: Acomys cabilinus (Egyptian spiny mouse)
Cispecies: Acomys cabilinus (Egyptian spiny mouse)
Cispecies: 13-13-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
Cidate: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
Cidates: Solding the Chem 353, 444-450, 1372
Riburalin H.F.: Humbel R.E.
Hopper-Seyler's Z. Physiol. Chem 353, 444-450, 1372
Altie: Isolation and partial structural analysis of insulin from mouse (Missuscitus)
A;Reference number: A01591; MUID:72189454; PMID:5026210
A;Reference number: A01591
A;Molecule type: protein
A;Accession: A01591
A;Molecule type: protein
A;Accession: A01591
C:Superfamily: insulin
C:Keywords: Hormone: pancreas
F;1-30/Domain: insulin exatus predicted cMAT>F;31-30/Domain: insulin chain A *status predicted
F;31-51/Domain: insulin chain A *status predicted
             PAFVNQHICGSHIVEALYINCGERGFFYTPK/FRREABDFÖVGQVELGGGFFGAGFIAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin procursor - Jack bear (fragments)
N.Alternate names: hypoglycemic agent; plant insulin
C.Species: Canavalla ensiformis (jack bear)
C.Date: 07-Dec-1999 %sequence_revision 07-Dec-1995 %lext.change 10-Fear-1999
C.Accession: BS9151, A59151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 FVNOHLCGSHIVEALYLVCGERGFFYTPKTRGIVSLOCTSICSLYGLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Cricerinae qun. sp. thamster;
Cispecies: Cricerinae qun. sp. thamster;
Cispecies: Cricerinae qun. sp. thamster;
Cispecies: Ag4456
Riveolon, F.A., Deloher, H.K.; Steinman, B.; Leberitz, H.E.
Fed. Proc. 32, 306, 1973
A.Title: Structure of harster insulin; nomparison with a tumor insuling Areterence number: A91456
A:Accession: Ag4456
A:Molecule type: protein
A:Residues; 1-20, 31-51 kNE>
C:Superfamily: insuling Cispering B status experimental engine C:Keywords: hormone; pancreas
F:1-30, 31-51/Product: insuling H status experimental engine F:1-30, 31-51/Product: insuling H status experimental engine F:7-37, 19-50, 35-41/Disulfide bonds: #status experimental engine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.3%; Score 271.5; DH 1: Jeugth
94.2%; Pred. No. 1.4e-21;
Uive 2; Mismatches o: Indels
                                                                                                                                                       EGSLOKRGIVEGCCTSICSLYGLENYCN 110
                                                                                                      -----RGIVEQCCTSICSLYQLENYCN 107
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Conservative
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Best Local Similarity 94.2
Matches 49, Conservative
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les 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               insulin - hamster
                                                                                                  98
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C:Species: Balacnoptera borealis (sci whale)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C:Accession: AC1582
R:Ishihara, Y.: Saito, T.: Ito, Y.; Fujino, M.
Retarc 181, 1468-1469, 1598
A:Thite: Structure of sperm- and sei-whale insulins and their breakdown by whale per A:Reference number: A93142
A:Reference number: A93142
A:Reference number: A03142
A:Residues: 1-30.31-51 <:SS-
                        Esulin procursor - chimpanzee
Cispcolos: Pan troglodytos (chimpanzee)
Cispcolos: Pan troglodytos (chimpanzee)
Cispcolos: Pan troglodytos (chimpanzee)
Cispcolos: Advar-1993 ascquence_revision 18-Nov-1994 *Lext_change 16-Jul-1999
Cispcolos: Advar-1993 ascquence_revision 18-Nov-1994 *Lext_change 16-Jul-1999
Riselao, S.: Bell, G.I.; 51, W.H.
Mail Biol, Evol. 9, 293-203, 1992
Advar-1998 *Advar-1998 *Adva
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C.Species: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C.Ancession: A01586
AE.Smith, L.E.
Am. J. Med. 40, 662-666, 1966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Tille: Species variation in the amino acid sequence of insulin. A.Reference number: A90029; MulD:66160119; PMID:5949593 AACCSSION: A01286 A.Residucs: protein A.Residucs: 1-30;31-51 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.5%; Score 267; DB 2; Length 110
60.5%; Pred. No. 9.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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CKeywords: hormone: pandreas

1-130/Commain: insulin chain B *status experimental cACH>

F:1-30.31 SI/Product: insulin *status experimental cACH>

F:1-51/Domain: insulin chain A *status experimental cACH>

F:2-37.19-50.36-41/Disulfide bends: *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 FVNOHLCGSHLVEALYLVCGERGFFYTPKT - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 ----RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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best Local Similarity
Matches 48; Cosserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 63/3
C;Superfamily:
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45.5%: Score 267, DB 1: Longth 110:
Best Local Similarity 60.5%: Pred. No. 9.36-21:
Matches 52; Conservative 0; Mismatches 5: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 FVNQHLGGSHLVEALYLVGGERGFFYTPKT - - -
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completed: September 15, 2003, 12:40:35 e.: 12:4903 secs
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[Cispedies: Camelus dromedatius (Arabian name)]
[Cispedies: Camelus dromedatius (Arabian name)]
[Cispedies: Camelus dromedatius (Arabian name)]
[Cispedies: 31-Mar-1992 *sequence_revision 51-Mar-1992 *t.ext__change 16-Juli-15-Juli
[Cispedies: A92782 | Repaired 14, 16-28, 1972 | Alither The isolation and characterization of insulin of came: (Camelus of mediation and characterization of insulin of came: (Camelus of mediation and characterization of insulin of profession: A92782 | Alither type: profession: A92782 | Alither type: profession: Assistant of the camelus of the c
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C.Species: Sus soroid domestica (domestic ptg)
C.Species: Sus soroid domestica (domestic ptg)
C.Species: Sus soroid domestica (domestic ptg)
C.Accession: A01563; A04572; S.C.4508.5; B60835
ByChance, R.E.; Ellis, R.M.; Bromer, W.W.
Science 161, 162-167, 1968
A.Title: Portine profissulin: characterizatic and amino ucid segmente.
A.Reference number: A04240; MUIT: 68286485; PMID: 5657065
A.Molecule type: protein
A.Residues: 1-34, '0', 36-64 <CHA>
Submitted to the A118s, July 1970
A.Molecule type: protein
A.Recidues: 1-84 <CHA>
A.Residues: 1-84 <CHA>
A.Residues: 1-84 <CHA>
A.Residues: 1-84 <CHA>
A.Residues: 1-80, 34 + 40
A.Recidues: 1-30, 31-51 <-ROS>
A.Rolecule type: protein
A.Residues: 1-30, 31-51 <-ROS>
A.Rolecule type: protein
A.Residues: 1-30, 31-51 <-ROS>
A.Rolecule type: protein
A.Residues: 1-30, 31-51 <-ROS>
A.Rolecule type: protein
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                                                                                                                                                                                                                                                                                                                      Score 263.5; DB 1; Length 51;
Pred, No. 9.6e-23;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                       44.9%; Score 263.5; DB 1; fength 90.4%; Pred. No. 9.6e-21; Live 1; Mismatches 3; Indels
C,Superfamily: insulin
C;Keywords: hormone; pancreas
F)1-30/Domain: insulin chain B fstatus experimental -BCE>
F)1-30/31-51/Product: insulin fstatus experimental -MAT>
F)31-51/Domain: insulin chain A fstatus experimental -ANG>
F)31-51/19-50,36-41/Disulilde bonds: fstatus predictud
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F11-30,31-51/Product: insulin Estatus experimental -RATY-
F31-51/Domain: insulin chain A Estatus experimental -ACHY-
F77-37,19-50,36-41/Disultide bonds: Estatus predicted
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Best Local Similarity 90.4%;
Matches 47; Conservative 1
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Matches 47; Conservative
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C)Superfamily: insulin
C)Reywords: hormone; pascroas
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A.Title: Proinsulin Actorogeneity in pigs.
A.Recession. 460835; MUD:89032178; PMID:3181865.
A.Accession. 460835; MUD:89032178; PMID:3181865.
A.Moiecule Lype: protein
A.Mosecule Lype: protein
A.Mos
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C.Seywords: hormone: pancreas
F:1-30/Donain: insulin chain B #status experimental <BCH>
F:1-30/Donain: connecting peptide #status experimental <MAT>
F:33-63/Donain: connecting peptide #status experimental <CPEP>
F:64-84/Zomain: insulin chain A #status experimental <ACH>
F:7-70,19-83.69-74/Zoisulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 84;
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GerCore version 5.1.6 copyright (c) 1393 - 2003 Compused Led.

Tue Sep 16 14:46:21 2003

OM protein - protein search, using sw model

September 16, 2003, 12:33:50 ; Search time 8:32685 Seconds (without algebrais) 604.29° Million cell updates/sear Run on:

US-09-423-100-6 567 1 MEPTIPLSRLFONAMIRANE......VEGTOTSFOSLYGLENYON 107 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 / Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127869 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summarres

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total shore distribution.

Result		% Query				
NO.	Score	Match	Length	60	G1.	Description
- 1	273.5		51	+ 1	INS_BALPH	halaen
7	273.5	46.6	51	~	INS_ELEMA	
3	273		1:0	-	INS_CERAE	
4	273		110	~	INS_MACFA	
Ŋ	268.5		51	-	INS_ACCCA	acomys
9	267		110	-	INS_HUMAN	
7	267	45.5	110	-	INS_PANTR	
80	266	45.3	CIT	_	INS_SPETR	sbor
δ	263.5		51	٦	INS_BALBO	
10	263.5	44.9	51	_	INS_CAMOR	
11	263.5	44.9	51	-1	INS_CAPHI	capro h
12	263	٠	10e	٠.	INS_PIG	S11S SC
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15	262	44.6	:10	٦	INS_CANFA	C3 URD
16	260		:10	٠.	INS_CRILO	P.C. 87 4 OF 109-046, 48-
1,	258.5	44.0	105	,	INS_BCVIN	P01917 Los tauris
18	257		108	,	INS_AOTIR	P10604 actus trivi
19	257		110		INS_PSAOB	062587 psammerys o
20	256.5	43.7	51	1	INS_DIDMA	Pl8109 didelphis m
21	255.5		217	-	SOMA_HUMAN	POll41 home Sapien
22	255.5		217		SOMA_MACMU	• •
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24	254.5		501	,	INS_SHEEP	POINT ONLS aries
25	252		30	٠,	INS_HOKSE	
56	251.5		5.1	, –	INS_CHIBR	
27	250		108	_	:NS1_MOUSE	P01325 mis mishuli.
28	249	42.4	110	-	INSI_RAT	2 : 41:
53	24.9	7	217		SOMA_CALJA	 e
30	543		217	-	SCMA_SA183	 55 36
31	248.5		51	-	INS_ANSAN	PC7454 amsor anser
35	248	42.2	1:0	-	INS2_MOUSE	
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എൻ നന	3.6 3.7	വാ ത തന	0	- 3	er • 5		in S

ALIGNMENTS

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MALTH 1NS_HALPH ST PC13612-1 21-501-1986 (Re: 21-501-1986 (Re: 11-501-1996 (Re: Insulfo. Insulfo. Insulfo. Engaryotera physical p	WCHILLIAKIE-19/70. 3 WCHILLIAKIE-19/70. 3 PARTIAL SEQUENCE. SEGLES-B-physalus Subcles-B-cados SEGLES-P-catodox; SEGLES-P-CATOGOX; SEGRES-P-CATOGOX; SEGRES-P-	SCCENCE SCORDER SECTENCE SECTENCE SECTENCE SECTENCE HERRIS J.I., Sander F., N TSPECIES differences in i Arch. Hicchem. Biophys. 6 -: FUNCTION: INSULIN DEC INCREASES CELL FERREA FATTY ACIDS. IT ACCELL FATTY BELCOGEN S: SUBCELLULAR LOCATION: -: SIMILARITY: BELCOGS TO PER ACIDS ACIDS: SIMILARITY: BELCOGS TO PER ACIDS.	HSSP: PO137: 1AN HSSP: PO137: 1AN InterPro: PR004 SMSATT: SS00278: PRCSTTE: PS0028: Inscitu family: Inscitu
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<u>.::</u>
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--- SGREELUGAR LOCATION: SECRETEG.
--- MISCELLANECUS: THE SPECIES OF FIEPHANT IS NOT GIVEN, BUT IT IS MOST PROBABLY THE INDIAN FIEPHANT (FIERMAS MAXIMES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa: Chordata, Craniata, Vertebrata, Eutoleostomi;
Mammalia, Eutheria: Primates, Catarrini; Cercopithecidae;
                                                                                                                                   56 FVNQHLGGSHLVBALYLVGGBRGFFYTPKTRGTVEQCCTS10S17QUBMYCY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elephas maximus (Indian elephant).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Proboscudea; Elephantidae: Elephas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 FVNQHLGGSHLVEALYLVGGERGFFYTPXTBGIVEQUOTSIGSGYGLENYCN 100
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                                                                                                                                                                FUNDHLOGSHIVBALYLVGGERGFFYTPRA-GIVEQCCTSICSLYQIENYCM ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 273.5, 08 1; Lenath 51;
Pred. No. 1,6e-22;
3; Kismatches (; indels )
                       DAS 13 CANGITY 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARHIY: BELONGS TO THE INSULINZIGEZERLAXIN FAMILY.
HSSP: P01308: 1A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.6%; Score 273.5; Ds.D. 96.2%; Pred. No. 1.69 22; Dive 0: Mismatches D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P30407; P01309;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FFB-1996 (Rel. 33, Last ennotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN B CHAIN.
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                                                                                                                                                                                                                                                                                                                                    Si AA
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SMART: SM00078: I1GF: 1.
PROSITE: PS00262: INSULN: 1.
                                                                                                                                                                                                                                                                                                                                       PKT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-66160119; PubMed-5949593;
                                                                                                                                                                                                                                                                                                                                                                                       01, Created)
01, Last seque
33, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.68;
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Conservative
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                               Best Local Similarity
Matches 50, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sest Local Similarity
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21-JUL-1986 (Rel.
01-FEB-1996 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Euther
NCBL_TaxID=9783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin family:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                                                                                                                                                                                                                                                                    INS_ELEMA
PC1316;
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DISULFID
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DISULFID
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                       Query Match
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DIT 21-JU

DIT 21
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1 INS
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no individed and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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23 PAEVNOHLOGSHLVEALYLVCGERGFFYTPKTRREAEDFOVGGVELGGGGGGGGGLGPLAL 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Procedure.";
J. Biol. Chem. 247.4866-4871(1972).
J. Biol. Chem. 247.4866-4871(1972).
J. Biol. Chem. 247.4866-4871(1972).
J. Biol. Chem. 247.4866-4871(1972).
J. PUNCHION: INSULIN DECREASES HIGDOD GLUCOSE CUNCENTRATION. IT
INCREASES CELL. PERMEDELLIT TO MONOSACCHRIDES, AMINO ACIDS AND
FAITY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-:- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                           Poterson J.D., Nebrlich S., Cyer P.E., Steiner D.E., "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                             MEDLINE-92219953: PubMed 1560757;
Setion S., Bell G.L., II W.,
"Sequences of primate itsilin genes support the typothusis of
slower rate of melecular evolution in humans and apes than in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 273; DB 1: i.ength 110; Pred. No. 4.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12019 MW; 95AlF54BE7B247F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone, Glucose metabolism, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INS_MACFA STANDARD; PRI; 110 AA. P30406; P01309; 21-301-1986 (Rel. Cl. Created) 1-7401-1987 (Rel. 05, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSULIN B CHAIN
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INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #3 EGSLOKHGIVEQUESIXOLENYON 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 -----RGIVEGCTSICSEYQLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR004825; Ins/IGF/relax.
Plam: PF00489; Insulin: 1.
SMART: SMC6078; IlGF: 1.
PRCSITE: PS00262; INSULIN: 1.
Insulin family; Hormone; Glucose me
                                                                                                                                                                                                                                                                                                                                                                          SECUENCE OF 57-87.
MEDLINE-72258016; PubMcd=4626369;
                                                                                                                                                                                                                                                                                                      Mol. Biol. Evol. 9:193-203(1992).
Sercept the cidae; Cercognihecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: X61092; CAA43405:1; -.
PTR: B42175; B42179.
HSSP: P01308; IAIG.
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60.2%:
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Watches 53: Conservative
                                                                                                SEQUENCE PROM N.A.
                            NCBL_TaxID-9534;
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82

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Mammalia: Eutheria: Rodentia; Sciuroguathi; Muridae; Murinae; Acomys.
NCBL_TaxID+10068;
                                                                                                                                                                                                                                                                                                                                                                                  Score 268.5: DB 3
Pred, No. 5.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
33-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                     INSULIN B CHAIN.
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                                                                                                                                                                                                                                                           PSD0262: INSULIN: 1.
amily: Hormone: Glucose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the human insulin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                   Interpro: IPR004825; Ins/INF/relax.
SMART: SM00078; INGE: 1.
                                                MEDLINE-72189454: PubMed-5028210; Buenzli H.F., Humbel R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                  45.7%;
                                                                                                                                                                                                                                                                                                                                                          5768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 209:612-515(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 282:525-527(1979).
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                          537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence of the human
Nature 284:26-32(1980).
                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin precursor
                                                                                                                                                                                                                                                                                                                                                           51 AA;
                                                                                                                                                                                                                                                           PROSITE, PSD0261
Insulin family;
                                                                                                                                                                                                                                                                                                2
                                     COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :NS_HUMAN P01308;
                                                                                                                                                                                                                                                                                              NON_COMS
                                                                                                                                                                                                                                                                                                                                              DISOLFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Obery Match
Best Tocal S
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                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Blobsformatics and the EREL outstaffed. The Burchean Blobsformatics Institute. There are no cretications on the use by non-profit institutions as long as its content, is in no way modified and this statement is not removed. Essays by and for commercial entities requires a license agreement (see http://www.isb-s.b.ci/stangement) or send as email to licenselish-sib.el).
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23 PAFVNOHLOGSHLVEALYSVOGESGEFYTPKTRREABDEGVOGVELGGGEGAGSLUELAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SdeO
                                                                                                                                                                  -:- FUNCTION: INSULIN DEGREASES BLOOD GLUCOSE CONCENTRATION. IT INREASES CELL PERREABILITY TO MONGSACCHARIDES. AKINO ACTIS AND FATTY ACTISS. IT ACCELERES CINCOLYSIS, THE PENTOSE PROSEHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVES. CYCLE, AND GLYCOGEN SYNTHESIS IN LIVES.
                                                                                            MEDINE-81080474: PubMed-6184262;
Wetckam W., Groneberg J., Leinowober M., Wengenmayer F.,
Winnacker B.-5.;
The nucleotide sequence of cDNA coding for preprolisation true
primate Macaca fascicularis.";
Gene 19:179-183(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acomys cabirinus (Egyptian spiny monse).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Eureleustom;;
                        Eukaryota, Motazoa: Chordata; Craniata; Vertebrata; Estelmostomi;
Mammalia; Eutheria; Elimates; Calarthin: Cercopitheridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~
            Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.5%; Score 273; DB 1: Length 110; 60.2%; Pred. No. 4.16-22;
                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Societed.
-1- SIMIDARITY: BELONGS TO THE INSCITUZION/MELAKIN PARTIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 PREVNQHICGSHLVEALY;VCGERGEFYCPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11991 MW; 83C5E33A80A420F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin family: Hormone, Glicose metabolism; Signal.
31GNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C PEPTIDE.
INSULIN A CHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN B CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RGIVEQCOISINGLENYON 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN
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PIR: J05178, J00178.
HSSP; P01308; LAIG.
InterPro: IPRC04925; Ins/IDS/relax.
Pram: PR00349; Ins01111.
PRINTS; PR00277; INSULINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01. Created)
01. Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00262; INSULIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD
                                                  Cercopithecinae: Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00078: 13F:
                                                                                                                                                                                                                                    SCINCE BOLLETOS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
01-NOV-1997 (Rel.
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43
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                                                            NCBI_TaxID: 9541
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Bignil H.F., Humbel K.E., mincoural analysis of insulin from mouse (Mus misciation and partial structural analysis of insulin from mouse (Mus miscius) and spiny mouse (Acomys cahirinus) ";
Hupper-Seyler's 2. Physiol. Chem. 353:444-450(1972).

i. FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES. AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS. THE PENTOSE PHOSPHATE (YCLE, AND SLYCOGSEN SYNTHESIS IN LIVER.

i. SUBCULT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY IWO
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Enkaryota Metazoa: Chordata; Craniata: Vertobrata; Euteleostomi;
Manmalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID+9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 FVNQHLCSSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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MEDLINE-80054775; PiDMed-503234;
Bultof W.J.;
Ruttof W.J.;
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MEDIINE-80120725; PubMed-6243748;
Medi G.I., Picter R.L., Kutter W.J., Cordell B., Tischer B.,
Goodman H.M.;
                                                                                                                                                                                                                                                                                                  DISCLEDE BONDS.
-!- SURCELULAR LOCATION: Secreted.
- SINICARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
- PIR: AC1541, IMMSSP.
HSSP: PC1908; ITYM.
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INTERCHAIN (HY SIMILARITY).
BY SIMILARITY.
992BDBB62964703D CRC64;
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A MEDLINE-22388257; PubMcd-12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derqe J.G., Atausberg R.L., Feingold E.A., Grouse L.H., Derqe J.G., Atausberg R.L., Feingold E.A., Grouse L.H., Derqe J.G., Bhat M. Altschul, S.F., Zeeberg B., Eutchow K.H., Schaerer C.F., Bhat M.K., Hopkins R.F., Jordan H., Mocre T., Max S.I., Wang J., Hsieh F., Altschul, S.F., Zeeberg B., Eutchow K.H., Schaerer G.F., Bhat M.K., Batchenon M., Soares M.B., Fondido M.F., Carning J.M., Hoog T., Brownstein M.J., Usdin T.H., Toshiyuki S., Carning J., Prange C., Raba S.A., McEwan P.J., McHenra K.J., Abramson R.D., Muliahy B.J., Bosak S.A., McEwan P.J., McHenra K.J., Abramson R.D., Muliahy B.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Hulyk S.W., Rodards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Hulyk S.W., Toshiyuki J., Myers M.A., Gubbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Goldiguez S., Sanchez A., Milladon D.K., Muly M., Madan A., Young A.C., Shevchenko Y., Goldiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska P., Smallus D.E., Schnerch A., Scher J.B., Jones S.J.M., Marra M.A., Generation and Initial analysis of more than 15,966 full-lenatt T. Proc. Natl. Acad. Sci. U.S.L., 99:16899-16903(2002).
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"Kb segment of DNA spannian the insulin gene and associated VNTR.";
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MEDLINE-71116410: PubMed-51(1771;
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MEDLINE-75040007: PubMed=48(3504;
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Nicol D.S.H.W., Smith D.F.;
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MEDLINE-87058122; PubMed=3537011;
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MEDLINE=85261996; Pubmed-4019786;
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MEDLINE-73161263; Pubned-4698555;
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                                                                              HopperSeyler's Z. Physiol.
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InterPro; IPR004825; Ins/IGF/relax.
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                                                                                                                                                                                                                                                                  "Comparative 2D NMR studies of human insuling and desepondangliable insuling sequential resonance assignment and implications for professionamics and receptor recognition.":

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assignment of a desepentabeptide analogue and comparison with organal
structure.":
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-I- SUBGNIT: HETERCOINSE OF A B CHAIN AND AN ALHAIN LINKED BY TWO
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Mammalia, Euthoria, Primates, Catarrhini, Hominidae, Pan.
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Seino S., Bell 0.1., 12 W.:
"Sequences of primate hall n genes support the hypothesis of
slower rate of molecular evolution in burans and apes than in
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Pred. No. 1.8e-21;
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01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                             MEDLINE-91104966; PubMed-2271664;
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Hua Q.-X., Weiss M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insulia precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                       STRUCTURE BY NMR.
                       STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Evol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID+9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INS_PANTR
P30410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monkeys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
INS_PANTR
10 2 93041
DT 01-APD
DT 01-APD
DT 15-SE
DT 15-S
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J.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way rouified and Lois statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 FVNQHICGSHIVEALYLVCGERGFFYTPKTRRBAEDLOVGOVELGGGFGAGSLOPLALEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tredrea M.M., Buck M.J., Guhaniyogi J., Squire T.L., Andrews M.T.,
"Regulation of PDK4 expression in a hibernating mammal.";
Submitted (JUN-2001) to the EXBL/GonBank/DBUJ databases.
-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHAIE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-!- SJBGNIT: HETTERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISGLEDE BONDS.
                                                                                                                                                                                                                SMART; SM06078; ILGF; 1.
PROSITE; PS00262; INSCLIN; 1.
Insulin family: Hormone; Glucose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41EB8DF79837CEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INS_SPETR STANDARD; PRT; 110 AA. 091X13; 15.5FP-2003 (Rel. 42, Last sequence update) 15.5FP-2003 (Rel. 42, Last annotation update) 15.5FP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                          INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.5%; Score 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 FVNOHIGGSHLVEALYLVGGERGFFYTPKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 SLOKRGIVEOCUSICSLYQUENYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 ----RGIVEQCCTSICSLYCLENYON 107
                                                                                                                                                                                                                                                                                                                                                    C PEPTIDE.
                                                                                               PDB: IEFE: 29-MAR-00.
InterFro: IFR004835: Ins/IGF/relax.
Pram: PF06049: Ins.Lin. 1.
PRINTS: PR00277: INSULINB.
SWART: SW06078: ILGF: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12025 MW;
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HSSP: PCL308; ILNP.
                                                  EMBL: X61089; CAA43403.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pest Local Similarity 60.5
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                    24
84
87
110
100
                                                                           PIR: A42179; A42179.
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57
90
31
43
110 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institu precursor
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dromedarius).";
J. Fdc. Med. Baghdad 14:15-28(1972).

-!- FJNCTION: INCULIN DECERBES BLOOD GLUCOSE CONCENTRATION. IT
:NCREASES CELL PERMEABILITY 10 MONOSACCHARIDES, AMINO ACIDS AND
FRITY ACCELERATES GLYCOLYSIS, THE PENIOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-!- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                Camelus dromedarius (Dromedary) (Arabian camel).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelusa; Camelus
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 FVNQHICGSHIVEALYIVCGERGFFYTPKIRGIVEQCCTSICSIYOLENYCN 107
   Danho W.O.; The isolation and characterization of insulin of camel (Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | FANOHIGGSHEVEALYZVGGERGFFYTPRA-GIVEGCASVCSLYQLENYCN 51
                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 263.5; DB 1; Length
Pred. No. 1.9e-21;
L: Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901E88BA085A7DDD CRC64;
                                                                                                                 21-57L-1986 (Rel. 01, Created)
21-57L-1986 (Rel. 01, Last Sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSULEN A CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insulin family; Hormone; Glucose retabolism CHAIN 130 INSULIN R CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004625; Ins/IGF/relax.
SMART: SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKT:
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-66160119; PubMed=5949593;
Smith L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.44,
Mest Local Similarity 60.44,
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                                                                                            STANDARD:
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37
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                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A92782: INCMA.
HSSP: P01317; ZINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AA:
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21-JUL-1986 (
01-FEB-1996 (
                                                                                          TNS_CAMDR
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
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                                                                                                                                                           Insulia.
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                                                                                INS_CAMDR
ID INS_C
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INS_CAPH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature 1811:468-1469(1958).

-1- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONDENTRALIEN, IT INCREASES CELL WONDSRACHARIDES, AMIN' ACHES AND FATTY ACIDS. IT ACCELERATES GIYCOLYSIS, THE PENTOSE PHOSENATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-1- SUBUNIT! HETERODIMES OF A B CHAIN AND AN A CHAIN LIKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  labihara Y., Saito T., Ito Y., Fujino M.;
Structure of sperm: and soi-whale insuling and their breakeam, by
Whale pepsin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Balachoptera borealis (Sel whale).
Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Butheria; Cetariticactyla; Cetacea; Mysticeti;
Balachopteridae; Balachoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ··.
                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1: Length Si;
                                                                                                                                                                                 Length 110:
                                                                                                                                                                 45.3%; Score 266; DS 1; Length, 113
57.4%; Pred. No. 2.2e-21;
Virgarches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN PARILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                 INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
4511768D6622BEBS GRG64;
                                                                                                                                                                                                                               50 LGTGP--REVNOHLGGSHIVEALYLVGGERGFFYTPKT------
                                                    metabolismo Siqual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9007B50E400A7DDD CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 263.5; DB 1;
Pred. No. 1.9e-21;
---t-hes 3;
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                                                                                                                                                                                                                                                                                 ------RGIVEOCCISICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1998 (Rel. 34, Last annotation update)
                                                                BY SIMILARITY.
INSULIN E CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN A CHAIN.
                                                                                         C PEPTIDE.
INSULIN A CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                       51 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART: SM00078: 116F: 1.
PROSITE: PS00252: INSTEAD: 1.
Insulin family: Hormone: Glucuse metabolism.
CHAIN: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO04825: Ins/iG:/relax.
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                       12004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.98;
92.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5723 MW;
             PRINTS: PRO0277; (NSULINS. SMART; SM00078; 11GF; 1. PROSITE; PS00262; INSULIN; Insulin family; Hordone; 63
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
Pfam; PF00049; Insulin;
                                                                24
54
87
110
96
109
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37
50
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HSSP; P01317; IAPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFIDE BONDS
                                                                                                                                                      11C AA;
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 48; Conserv
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57
50
51
51
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P01314;
                                                                                                                                                                               Query Match
Best Local Simi
Matches 54;
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SEQUENCE.
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CHAIN
                                                                                                                                        DISULFID
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                                                                                                                              DISULFID
                                                                                                                                                      SEQUENCE
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                                                                             CHAIN
                                                                 SIGNAL
                                                                                                     CHAIN
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INS_BALBO
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Gaps

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112B;
2TCI;
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3MTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :DEI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 I NS ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SINS;
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PD3;
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PDB;
PDB;
PPB;
PDB;
PDB;
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PDB;
PDB;
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PDB;
PDB;
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            AM. J. Med. 40:662-665(1965).

*!*FUNCTION: INNULIN DECREASES BLOOD GLUCOSE CONCENTRATION, IT INCREASES CELL PERMEAB-ILTY TO MONOSACCHARIDES. AKING ACTIS AND FATTY ACIDS. IT ACCELERATES GLYCOCYSIS, THE PENTOSE PROSHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

**SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative sequence analysis of the INS IGF2-819 gene cluster in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 FVNQHLGGSHLVEALYLVGGRRGFFYTPXTRG1VHJCGTS10SLYQDANYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entologs om;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-68286485; PubMed 5657063;
Chance R.E., Ellis R.M., Bromer W.W.;
*Portine proinsulin: Characterization and amino unid sequence.";
Science 16::165-167(1968).
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MEDLINE=22135958; PubMed-1214C686;
Amarger V., Ngiyen M., Laeke A.S., Braunschweig M., Nezek C.,
Georges M., Andersson L.;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 263.5: De la Lonata Sta
"Species variation in the amino acid sequence of insulin.";
                                                                                                                                  -:- SUBCELLUTAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULINTICE/RELAXIN PAMILY.
PIR: A01586. INST.
HSSP, P01317. IAPH.
                                                                                                                                                                                                                                                                                                                                                                                                                             (90-21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Han X.G., Tuch B.E.;
"Complete possible proproinsalin cENA sequence.":
Submitted (MAY-1998) to the EMBL/Genbank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                           9007B50CD84E7CDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metázoa, Chordata, Graniata, Vertebruta.
Mammalia, Eutheria, Cetartiodactyla, Snina, Suidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS),
Blundell T.L., Fodson G.G., Hodgkin D., Mercela fo.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01315, 057835;
21-302-1986 (Rel. 01, Created)
10-007-2001 (Rel. 40, Last Sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                         INSULIN A CHAIN.
INTERCHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                         INSCILN B CHAIN.
                                                                                                                                                                                                                                       PROSITE: PS00262; INSULLN: 1.
Insulin family: Hormone: Glucose metabolism
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1.
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SMART: SM00078: ILGF: 1.
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41
6692 MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               47: Conservative
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                                                                                                                   DISULFIDE BONDS
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Chance 9.E.:
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the Buropean Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb~sib.ch/announce/
or send an email to license@isb~sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        baker E.N., Biundell T.L., Cutifeld J.F., Cutfield S.M., Dodson E.J., Dodson G.G., Growthort Hodgkin D.M., Hubbard R.E., Isaacs N.W., Reyrolds C.D., Saxabe N., Vijayan N.M., "The structure of 222 pig insulin crystals at 1.5-A resolution."; Philos. Trans. R. Scc. Lond., B, Biol. Sci. 319:369-456(1969).
                                                                                                                                                                                    Isaacs N.W., Agarwal R.C.;
"Experience with fast Fourier least squares in the refinement of the crystal structure of rhombohedral 2-zinc insulin at 1.5-A resolution.";
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"Structure of monomeric porcine DesB1-B2 despentapoptide (B26-B3C)
insulin at 1.65-a resolution.";
Acta Crystallogr. D 53:507-512(1997).
-!-FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMING ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOSEN SYNTHESIS IN LIVER.
-!-SUBDINT: HETEROLIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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WWW-"http://www.expasy.orq/spctlight/articles/sptit009.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDSAINE-$1222450; PubMod-2025410; Badger J., Harris M.R., Reynolds C.D., Evans A.C., Dodson E.J., Dodson G.G., Morth A.C.T., Structure of the pig insulin dimer in the cubic crystal."; Acta Crystallogr. B 47:127-136(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X. RAY CRYSTALLCGRAPHY (2.0 ANGSTROMS).
MEDLINE=92126286; PubMed-1772633;
Ralschmidt P., Hansen F.B., Dodson E., Dodson G., Korber F.;
Structure of parcine insulin cocrystallized with clupeine R.;
Acta Crystallogr. B 47:975-986(1991).
"Insulia, The structure in the crystal and its rellection in chemistry and biology.":
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SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DATABASE: NAME-Frotein Spotlight;
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                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
MFDLINE-69099318; PubMcd-2905485;
                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
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                                                                        Adv. Protein Chem. 26:279-462(1972).
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16-FEB-99.
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SUBUNIT: HETEROI
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110 AA;
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es 51: Conserv
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SIGNAL, 1 24
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Eukaryota, Metazoa, Chordata: Craniata, Vertebrata: Entoleostomi:
Mammalia: Eutheria, Lagomorpha, Leporidae: Oryctolagus.
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MEDIARE-94179230; PubMed-8122571;
Devaskar S.U., Gladdings S.J., Rajakumar P.A., Carnethi D.R.,
Kenon, R.K., Zahm D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 263; DR 1: Length 108:
Pred. No. 4.5e-21;
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Am. J. Med. 40:662-666(1966).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
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| HILL | HITTHELTTH
| 85 QKRGIVEQCOTSICSEXQLENYON 108
                                                 InterPro: 1PR004825: Ins/IGE/reldx.
Pfam; PF06649; Insulin; 1.
SMART: SM06078; IIGE; 1.
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MEDLINE=66160119: PubMed-5949593:
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P01311;
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
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Brantyotus Metazoa, Chordata: Craniata; Vertebrata; Euteleostomi;
Marmalia: Euteria; Carnivora: Pissipedia: Felidae; Felis.
NGELTAXID-9605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1; Length 110; 4.6e-21;
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E -> Y (IN REF. 3).
82D2975885D77FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Mormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51-JAN-1986 (Rel. C6, Created)
61-JAN-1988 (Rel. 26, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 ALOKRGIVEQCCTSICSLYQLENYCM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 ----RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPIIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                      PTR, A53438; INRB.
HSSP: P0:308; ITYM.
THEEPED: IPROC4825; INS/IGE/relax.
Piam: PPOUG49; Insulin: 1.
SMART: SMO078; IIGE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR: AC1583; INCT.

1858: POL317; IAPH.

InterPro; IPRO04825; INS/IGF/relax.

PRINTS; PRO0277; INSULINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJINE=86214076; PubMed-3518635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11838 MW;
                                                                                                                                                                                                                              EMBL: 003610; AAA19033.1; -.
EMBL: M61153; AAA17540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.8%;
ilarity 59.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                 SMART: SM00378; IlGF; l.
PROSITE; PS00262; INSULIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
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54
87
110
109
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                                                                                                                                                                         _
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE-83109971, PubMed-6296142:
Kwok S.C.M., Chan S.J., Steiner D.F.;
"Cloning and aucleotide sequence analysis of the dos insuling and
Coded amino acid Sequence of canine preproinsuling predicts an
additional C-peptide fragment.":
J. Biol. Chem. 258:2357-2363(1983).
                                                                                                                                                                                                 56 PVNQHLGGSHLVBALKIVJGBRGFFYTPRTRGIVGGYTYTSTJSLYÐLENVYN 107
171-111: (1111 - 1111 - 1111) - 1111 - 1211 - 131
I EVNQHLGGSHLVBALKIVJGBRGFFYTPRA-GIVGGYTASVJSLYÐJEHYGN 51
                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Nos).
Eukaryota: Metazos, Chordana, Cramiata: Metroratu: Dutuleosteni:
Mammalia: Euthoria: Carnivora, Fissipedia: Canidae: Canis.
                                                                                                                                                                         1;
                                                                                                                                               is likesyth 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS.
-:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                        2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, V00179; CAA23475.;; -
PIR, A92413; :PCA
FIRSP, P01417; 1APH
InterPro; TPR004825; IUS/IGF/relax,
PR00484; INSUID; 1
SMART; SM00076; IIGF; 1
PROSTE: PS00262; INSTIN; 1.
Insulin family; Hormone; Glucose motabolism: Signal.
                                                                                                                     9007B5096A0A7DDD CRC64;
                                                                                                                                              Score 262.5: DB : Pred: No. 2.4e+21:
                                                                                                                                                                                                                                                                                                                 21-001-1986 (Rel. 01, Created)
21-00L-1986 (Rel. 01, Last Sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
SMART: SMC0C78: ILCF; 1.
PROSITE: PS00262; INSULIN: 1.
CIRRLIA: family: Hormone; Glucose metabolism..
CIRRLIA: 30 INSULIN B CHAIN.
                                                                   INSULIN A CHAIN
                                                                                                                                                                                                                                                                                            110 AA
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                                                                              INTERCHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                            PRT;
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SEQUENCE OF 25-54 AND 90-110.
MEDLINE-66160119; PubMed-5949593;
                                                                                                                                            44.78;
90.48;
                                                                                                                    5745 MW;
                                                                                                                                            Ouery Match
Best Local Similarity 90.44
Matches 47; Conservative
                                                                                                                                                                                                                                                                                            STANDARD:
                                                    51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                              NGB1_TaxID-9615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith L.F.;
                                                                                                                                                                                                                                                                                            INS_CANFA
                                                    NON_CONS
CHAIN
                                                                                           DISULFID
                                                                                DISULFID
                                                                                                                     SEQUENCE
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GenCore version 5.1.6
Copyright (c) 1993 - 2603 Compugen 1.dd.
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OM protein - protein search, using sw model

September 16, 2003, 12:34:00 ; Swarch time 25:81:2 Seconds (without alignments) 1669:670 Million cell updates/seconds Run on:

US-09-423-100-6 587 1 MEPTIPLSRLEDNAMIRAGE......IVECODISIOSLYGGENYGN 107 Title: Perfect score: Sequence:

Scoring table:

HLUSCM62 Gapor 10.0 . Gapext 0.5

830525 segs, 258052604 residues Scarched:

830525

Minimum DB seq length: 0 Maximum DB seg length: 2000005000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

.. Database

SPTREMBL_23:*

spontancile:
sp_phage:
sp_phant:
sp_rodent:
sp_virus:
sp_virus:
sp_virus:
sp_rvirus:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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SUMMARIES	Q:	Q8HXV2	Q91XT3	QBWNW6	OBWNE0	014644	091807	C07368	C07367	098788	007369	014407	090085	0.502N4	098TB0	50NMBO	Q902Y1
	53	9	7	9	ç	-	13	(y)	ω	13	ıc	77	~1	٠,	; e. ; - 1	ç	33
	* Ouery Match Length DB	011	CLI	0.11	217	245	106	2:2	2:7	110	217	217	108	0.1		2:7	1:0
:	% Ouery Match	45.5	45.3	42.8	42.4	38.8	37.4	36.3	35.3	34.3	34.2	33.6	3 \$. 3	33.3	3.3.2	33.2	33.0
	Score	267	266	251	249	228	219.5	213	213	201.5	201	197	195.5	195.5	195	195	193.5
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0981A7 0981B1 0981A9 0981B2 08M174	C70615 Q9TV91 Q8M173 Q8MY73 Q9RXE5 Q9R2C3	095835 095205 08AV14 093607 073720		
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13 18 20 20 21	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. 8 5 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 4 6 8 4 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	○ ं हें है ने के च च च च च च च

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RESULT OFBXV2	-		;	
2 ¥	HXV2	PRELLMINARY:	PRT;	110 AA.
5	2003	23,	Created)	
5	01-MAR-2003 (TrEMBLrel.	23,	Last sequ	Last sequence update)
E	01-MAR-2003 (TrEMBLrel)	23,	Last anno	Last annotation update)
10 01	Insulin precursor.	rsor.		
S	INS.			
S	Pongo pygmaeus	Pongo pygmaeus (Orangutan).		
9	Eukaryota; Met	Cazoa: Chordata	; Craniat	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
8	Mammalia; Eutheria;	meria, Primates;	; Catarrh	Catarrhini; Hominidae; Pongo.
č	NCBI_TaxID -9600;	00;		
Z.	[1]			
ŭ,	SEQUENCE FROM N.A.	N.A.		
Æ,Y.	Stead J.D.H.,	Jeffreys A.J.;		Stead J.D.H., Jeffreys A.J.;
E.	"Haplotype div	rersity at the	insulin r	egion.";
.4	Submitted (JUL	2002) to the	EMBL/GenE	ank/CDBJ databases.
ж Э	EMBL: AY137503	EMBL: AY137503; AAN06937.1;		
Ģ.	SEQUENCE 110) AA; 12038 KW	; 22D2B3	110 AA; 12038 MW; 22D2B32B94F520F8 CRC64;
ō	Cuery Match	ef in ur *7	Score 26	Score 267: DR 6: Tenath 110:
ň	Best Local Similarity		Pred. No	
ž	Matches 52; Co	vative	0; Mismatches	tches 0; Indels 34; Gaps
40	HONAL 95	HLCGSHI,VEALYLVC	GERGFFYTF	56 FVNQHLCGSHI,VEALYL,VCGERGFFYTPKJ
				_
3	25 FVNQH	HICGSHLVEALYLVO	GERGFFYTP	FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLOVGOVELGGGPGAGSLQPLALEG
Š	86R	RGIVEQCCTSICSLYQLENYCN 107	CLENYCN 1	40
	_		1 1 1 1 1 1 1	
ŝ	85 SLOKR	85 SLOKKGIVEQCCISICSLYQLENYCN 110	OLENYCN :	10

ä 8.5 84

110 AA.

PRT;

G91XI3; 01-DEC-2001 (TrEMBLES), 19, Created)

PRECEMINARY:

RESOLT 2 Q91XT3 1D Q91XT3 AC C91XIN; ET 01-DEC-2

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Euteleostomi;
Atelinac: Ateles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Term placenta;
MEDGINE=983737; PubMed-9709963;
Boquascawski C.L., Svensson P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
"Clocing of two novel growth hormone transcripts expressed in human placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HORD Sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
NCBL_TaxID=9506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FPTIPLSRLFUNAMLRAHRLHQLAHDIYQEFEEAYIPKEQKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 42.4%; Score 249; DB 6; Longth 217; Bost Local Similarity 97.9%; Pred. No. 2c-21; Matches 47; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frank, Frozzo), Mormon, 1.
PROSITE; PS00266: SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
SEQUENCE: 217 AA: 24894 MW; 425829FF41EEAAF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
14CC7F8CD75D91C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eskaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-5AN-1998 (TrEMBLrel. 05, Created)
01-5AN-1998 (TrEMBLrel. 05, Last sequence update)
01-0EC-2601 (TrEMBLrel. 15, Last annotation update)
Plucental growth hormone isoform hGH-V3 precursor.
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Clin. Endocrinol. Metab. 83:2878-2885(1998).
EMBL: AF006061; AAB71829.1; -.
HSSP: P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atches geoffroyi (Black-handed spider monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA.
                                                                                                                                                                                                                                             217 AA
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                                                                     95 PLOKRGIVEGCGASVOSINQLEHYGN 110
                                          36 ----RGIVEGGCTSICSINGLENYCN 107
                                                                                                                                                                                                                                                                                                      Created)
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PROSITE: PS00266; SOMATOTROPIN_1; 1.
                                                                                                                                                                                                                                             PR
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                                                                                                                                                                                                                                                                                                01-MAR-2602 (TrEMBLrel. 20, 
01-MAR-2602 (TrEMBLrel. 20, 
01-MAR-2603 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.88;
                                                                                                                                                                                                                                             PRECEMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_Tax1D+9509;
                                                                                                                                                                                                                                                                                                                                                                                       Growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE
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SignAl
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Tredrea M.W., Buck M.J., Guhaniyogi J., Squire T.L., Andrews M.T.:

"Regulation of PDK4 expression in a libernating mastal.";

"Submitted (JUN-2001) to the EMBL./Genbank/NDB3. databases.

-1- SUBCELIJLAR LOCATION: SICKNEIPED (BY SIMILARITY).

-1- SUBCELIJLAR LOCATION: SICKNEIPED (BY SIMILARITY).

REMBL: AKO38604; AAK72558.1;

REMBL: AKO38604; AAK72558.1;

RISSP: PO1306; LLNF.

RISSP: PO1306; LLNF.

R FRINTS: PRO0495; Insulin: 1.

R PRINTS: PRO0495; INSUlin: 1.

R PRINTS: PRO0778: INSULIN: 1.

R PROFITE: PS00262; INSULIN: 1.

R PROSITE: PS00262; INSULIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 LGTGP--RYVNQHLCGSHLVEALYLVCGERGFFYTPKT-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felis silvestris catus (Cat).
Eukaryota: Metazoa, Chordata, Craniata: Vertebrata, Enteleostomi:
Mammalia, Butheria, Carnivora, Fissipedia: Polidae, Felis.
                                                                                    Spermophilus tridecorlineatus (hirteen-lino) mound squirto)
Bukaryota: Motazoa: Chordata: Gramiata, Vattebrata; Enteleostorio
Marmalia: Eutheria: Rodentia: Sciuroquathi: Sciuridse: Sciuinee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.3%; Score 266; DB il: Arngth 110; 57.4%; Prod. No. 8.7c-24; ive 1; Mismatches 3: Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.8%; Score 251; DB 6: Langth 110: 55:8%; Pred. No. 5.36-22: tive 2: Mismatches 2: tade!s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2000) to the EMBL/Conhank/DPB) dutahases.
-1. SUBCELULAR LOCATION: SICRETED (BY SIMILARITY).
-1. SIMILARITY: BELDNGS TO THE INSULIN/TOF/RELAXIN FAMILY.
EMBL: AB041553: NAB84110.15. -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 FVNQHLGGSHJVBALYLVGGRRGFFYIPKI----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: 1PR004625; Ins/10F/relax.
Pfam: PF00049; Insulin: 1
PRINTS; PR00277; INSULINS.
SMART: SM00078; ILGE: 1
SMART: SM00262; INSULIN: 1; SEGUENCE: 110 Aa; 12069 MW: 95FB6EI70c73BECAT CRC64;
01-DEC-2001 (TYBMHLFG), 19, Last sequence update; 01-MAR-2003 (TYEMBIRE), 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: MAR-2002 (TrEMBLrol. 20, Created)
01-MAR-2002 (TrEMBLrol. 20, Last sequence update)
01-MAR-2003 (TrEMBLrol. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 PQPLALEMALQKRGIV5QCTSICSLYQL5NYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.0 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.00,
And 48, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.4%
Matches 54; Consorvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Pancreas:
Okamoto S., Morimatsu M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                        Spermophilus.
NCB:_TaxID-43179,
                                                                                                                                                                                                                                                                                             TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_Tax10+9685;
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110 AA.
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                                                                                     InterPro, IPR001400; Somatotropin, Plam: PF00103; hormone: 1. PROSITE; PS00338; SONATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chorionic somatomammetropin-1.
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINIS, PROOB36, SOMATOTROPIN.
PROSITE, PSOOB38, SOMATOTROPIN.
                                EMBL: L16553; AAA18840.1: -. HSSP: P01241; TAXI.
                                                                                                                                                                                                                                               Owery Match
Best Local Similarity 78.7%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 78.7
Matches 37, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: 016552; AAA18
HSSP; P01241; LAXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEÇUENCE FROM N.A.
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007367
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                                                              Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Kanidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa, Chordata: Craniata, Voitebrata, Euteleostomi;
Mammalia: Eutheria, Primates, Catarrhini; Cercopithecidae,
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                                                                                                                                           2 PPTIPLSRLFDNAMLRAHRLHQLAFDTYQRFEEAYIPKHCKYSFLONP
4: Inde:s
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01-NOV-1996 (ITEMBLICE). 01, Last sequence update)
01-MAR-2003 (TTEMBLICE). 23, Last annotation update)
Somatotropin 2 precursor (Grewth hormone 2) (Fradment).
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AA: 12183 MW: 3A870EEG76217F32 GR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana pipiens (Northern Leopard frog).
Eukaryota: Metazoa: Chordata; Craniata: Vertabrata:
Amphibia; Batrachia: Anura: Neobatrachia; Rasoides:
                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                   3.06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 KPGIVEQCCHUTCSLYDLENYCN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20362507: PubMed-10318274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94008724; PubMed-8434617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00262; INSULIN; :
                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2060 (TrEMBLrel, 15, 01-OCT-2060 (TrEMBLrel, 15, 01-MAR-2063 (TrEMBLrel, 23,
                                                        44: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
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NCBI_TaxID=9544;
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                             Best Local Similarity
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Q07358;
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                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUN=Xidoressancy placenta; MEDINE=54.0872 (200724; PubMed-8404617; Gelos T.G., Durring H., Fisher P.D.; Colosing of four growth formone/chorinoic somatomammotropin-related complementary dooxyribonucieic acids differentially expressed during prequency in the rhesus monkey placenta."; Endocrinology 133:2744-1722(1993).
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota: Metazoa, Chordata: Craniata, Vertebrata, Euteleostomi:
Mammalia: Butheria; Primates, Catarrhini, Cercopithecidae,
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pantodon buchholtzi (Butterfiyfish).
Sukaryota, Metazoa; Chordata, Craniata: Vertebrata: Buteleostomi;
Actinopterydii: Necpterydii: Teleostei: Osteoglossomorpha;
Ostcoglossiformes: Pantodontidae; Pantodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.3%; Score 213; DB 6; Length 217; 78.7%; Pred. No. 3.8e-17; Live 9; Mismatches 1; Indels
                                                                                                                                                                                        3 PTIPLSRLFONAMLRAHRLHQLAFDTYQEFEEAYIPKFQKYSFLQNP 49
                                                                                                                                                                                                                             23 PSVP.SRLFDHAMIQABRAHQABADTYQEFESAYIPKEKKHSLMENP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 212;
                                                         36.3%; Score 213; DB 6; Length 21
78.7%; Pred. No. 3.7e-17;
Live 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-21203577: Pubmed-11306171;
Al-Mahrouki A.A., Irwin E.M., Graham E.C., Youson J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24942 MW; FF5AA8915131F2BC CRC64;
SEQUENCE 212 AA; 24525 MW; 27BC91106256E6F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1 NOV-1996 (Tremshrel, Gl, Created)
01-NOV-1996 (Tremshrel, 01, Last sequence update)
01-MAR-2003 (Tremshrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBirel. 17, Created)
01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
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us-09-423-100-6.rspt

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MEDLINE-89307277; PubMcd-2744760;
Clen E.Y., Liac Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanic rerio (Zebrafish) (Danio rerio).
Bukasyota: Metazoa, Chordata, Craniata: Vortebrata; Buteleostomi;
Actisopterygii: Neopterygii: Teleostel: Ostariophysi; Cypriniformes;
Cyprinidae: Danio.
                                                                                                                                                                                                                                    The human growth hormone locus: nucleotide sequence, biology, and
                                                                                                                                                                                                                                                                                                                                               MEDCINE=91102958; PubMod-1980158; Whencak-Ones C.L., Phillips J.A. III.; Whencak-Ones C.L., Phillips J.A. III.; Whencak-Ones C.L., Phillips J.A. III.; outside of Alu repeats.
                                               Eukaryota, Melazoa, Chordata, Cranhata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Argenton F., Zecchin E., Bortolussi M.;
"Darly appearance of pancreatic hormone-expressing cells in the zebrafish embryo.";
"Statish embryo.";
"Hebrish embryo.";
"ESUBCELLULAR DOCATION: SECRETED (BY SIMILARITY).
"SUBCELLULAR DOCATION: SECRETED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.6%; Score 197; DB 4; Length 217; 85.6%; Pred. No. 3e-15; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24994 MW; 39FAACDDB6B2E951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Greated)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hast, receptor, interpretable somatctropin.
Pram. PF00103; hormone; 1
PRINTS; PR00884; SOMATCTROPIN.
PROSITE; PS00266; SOMATCTROPIN.; 1
PROSITE; PS00388; SOMATCTROPIN.; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL-2002) to the EMBL
EMBL; 903071; AAA52553.1; -.
EMBL: BC022044; AAH32964.1; -.
EMBL; BC035965; AAH35965.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 250:1745-1748(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 80.03
les 36, Conservative
                                                                                                                                                                                                                                                                                 Genomics 4:479-497(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELEMINARY:
         2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-7955,
                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                       Chen E.Y., L18
Seeburg P.H.;
                                                                                                                                                                                                                                                       evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECTIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Q90085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
990085
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         8
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                                                                                                                                                                                                                                                                                                                                                                                                                    : TITTELTITELTETT : TITT : TIT : TIT : TIT : TIT : TIT : TITT : T
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01-NOV-1996 (TrEMBLrel, 01, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
Chorionic somatomammotropin CS-2 (Chorionic sematomammotropin hormone
                                                                                                                                                                                                                                                                                                                                                   Side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Golos T.G., Durning M., Fisher J.M., Fowler P.D.,
"Closing of tour growth hormone/Chint's comalcommontropin-related
"Closing of tour growth hormone/Chint's comalcommontary decayrishopurelets a cids differentially expressed during
pregrammy to the rhosus monkey placental";
Endocarino.comy 133:1744-1752(1993).
EMBL: L16554: AAA.1841.1.
ESSP; P01241: IAXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Eutoleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                 Ę,
                                                                                                                                                                                                                                                                                                  34.3%; Score 201.5; DB is: Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSVPLSREEDLIMMOAGREHOLAFOTYOGERKTYIPKEKKGSJAGNP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PTIPLSRLEDNAMLRAHRLEQLAFDTYGSFFERAYLFKEGRYSFLGNF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%; Score 261; Ds 6; Length 217; 74.5%; Pred, No. 1e-15;
                indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIEBSAFDRBAIBI85 CRC64;
"Molecular cloning of preproinsulin combs from several
                                                                                                                                                                                                                                                       3DEGCD659D872E06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
(1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
(1-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Chorizonic somatcomarmotropin.3.
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                            ٠.
                                                                                                                                                                                                                                                                                                                     Pred. No. 4e-16;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---RSIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 KVKRGIVEQCCHHPCNIFDLQNYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro/ IPR001409: Somatotropin.
Pfam: PF00103; hormone: I
PR003TE; P000266: SOMATOTRO:IN. 1: 1.
SEQUENCE 217 AA: 24874 MM: FIERES
                                                                                                                                                     InterPro, 7RR04825: Ins/13F/relax.
Pfam: PF00049: Inschin: 1.
SMATT: SM00074: 10FF: 1.
PROSITE: PR00525: INSCLIN: 3DE03
SEQUENCE 110 AA: 12324 MM: 3DE03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE Midpregnancy placents;
MEDLINE-94008724; Pubmed-84(4617;
                                                                                                                                                                                                                                                                                                                     43.5%;
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.5
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207369;
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Q14407
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50
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Gaps

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26 NGHLGGSHLVEALYLVGGERGFFYNPKMDKRDAEPLLGFLSPKSGLENEVDEYPFKDQGD 85
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Mammalla, Butheria, Primates, Platyrrhini, Cebidae, Atelinae, Ateles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                       Eukaryota: Metazoa, Chordata, Crâniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Osteoglossomorpha;
Gsteoglossiformos; Notopteridae; Chitala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ċ
                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A. Requivel D., Santiago D., Rarrera-Saldana H.; Revol A., Esquivel D., Santiago D., Rarrera-Saldana H.; Independent displication of the growth hormone gene in three Anthropoidean ilmeages."; Submitteed (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL: 3734235; AAL722R7.1: 'InterPro: IPR001406; Somatctropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.2%; Score 195; DB 6; Length 217; 77.1%; Pred. No. 5.2e-15; Live 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 NQHLCGSHLVKALYLVCGERGFFYTPK-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         indels
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Primrs; PR00836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.1; 1.
PROSITE; PS00388; SOMATOTROPIN.2; 1.
PROSITE; PS00338; SOMATOTROPIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 111 AA; 12483 MW; 2470A4431376329F CRC64;
                             61-JON-2001 (TrEMBLrel. 17, Created)
01-JON-2001 (TrEMBLrel. 17, Last sequence update)
19-PAR-2003 (TrEMBLrel. 23, Last annotation update)
Preproinsulin (Fragment).
Chitala chitala (clown knifefish).
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51-NAR-2002 (TrEMBLIEL, 20, Last sequence update)
61-0cT-2002 (TrEMBLIEL, 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.2%; Score 195: DB 13:
44.2%; Pred. No. 2.4e-15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ateles geoffroyi (Black-handed spider monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 AA
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Matches 37; Conservative 5; Mismatches
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86 VKMKRGIVEQCCHRPCNIFDQNQYCN
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Sest Local Similarity
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Ostariophysia Cyprin'fordes:
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INSULIN B CHAIN.
INSULIN A CHAIN.
3195283E72AD6D25 CRC64:
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01-5EC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
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Bukaryota: Mctazoa: Chordata: Craniata;
Catlanopterydii: Neop.erydii: Teleos.ei;
Cyprinidae: Catla:
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RGIVEOCCHEPCSIFFELONYON 108
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                          HSSP; P01308; 1LPH;
ZFIN; ZCB-GDNE-966526-110; ins.
InterPro; IPR004655; ins/IGF/relax.
Pfam; PF00049; insulin; 1.
PRINTS; PR00277; INSULINB;
SMART; SMC0C78; I1GF; I.
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Pfam: PF00649; Insulin; 1.
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EMBL; AJ237750; CAC20109.1; -.
                                                                                                                                                                       SMART; SMCGC78; T1GF; 1,
PROSITE; PSG0262; INSULIN; 1.
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SMART; SM00078; ITGE; 1
PRCSITE; PS00262; INSULIN: 1
SEQUENCE 108 AA: :1881 MR:
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Matches 37: Conservative
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01-MAR-2003 (TremBirel.
Preproinsulin.
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108 AA;
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nes 37; Conserv
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SIGNAL
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27 FPRIPLSRDFGDAMLRAHGUAQVAPDIYQELEENGIPKKÇKTIFTIRNE 74

Search completed: September 16, 2063, 12:40:00 Job time: 27.8132 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compuges std.
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	September 16, 2003, 12:31:20 ; Search time 44.358 Seconds (without allements)
₩ model	12:31:20
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search,	mber 16,
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Title:	US-09-423-100-7
Segmence:	1 MEPTIETSRIFUNAMIRAHRtvEgchtsicslyglenycw 150
Scoring table: BLOSCM62	BLASCM62 Ganob 10 0 . Ganext 0 5
Searched:	1.07865 sees. 158726573 residues

1107863 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match (% Maximum Match 100% Listing first 45 summaries Databa

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Chimeric protein. 55H-min:protein. Human growth horror Human growth horror Human growth horror Human growth torror Human growth torror Human growth torror Human growth hormor
SUMMARIES	AAY 12851 AAY 12856 AAY 12856 AAY 12856 AAY 1295 AAY 129 AAY 129 AAY 104:
PG FG	20 20 20 20 20 20 20 10 10
% Query Match Length DB	150 1020 1334 1321 1460 261
% Query Match	100.0 69.7 59.7 59.0 58.3 58.3 58.3 58.3
Score	5 5 5 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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Human growth hormo Fusion protein of Mature human growt Human growth hormo Segment of B-cell	growth growth beta-ner in seque al human growth	growth growth growth growth	growth growth growth growth growth growth growth	growth growth growth growth growth growth growth growth
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ALIGNMENTS

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insulin; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant; production; yield.
                                                   AAY42861 standard: protein; 150 AA.
                                                                                                                                                                                                      Chimeric protein, 850 ID 7.
                                                                                                                                                   19-JAN-2000 (first energy)
                                                                                                      AAY42861;
RESULT 1
AAT42861
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25000ND-CM86 Homo sapiens. W09950302-A1 31-KAR-1998; 07-0CT-1999. Synthetic.

(TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD. Can 2;

98WO-CN00052.

31-KAR-1998;

New chimeric proteins containing human growth hormone fragment, used WELL 1999-610839/52.

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This sequence represents a chimeric protein, which contains an N-terminal tragment of human growth hormone (bHB) of the sequence growed in AAV42856, and cleavable peptide linear (AAV42859), and sharin insulfs procursor compising itsulfs the chimeric protein acts as an intramolecular chaperone (IMC) for the chimeric protein acts as an intramolecular chaperone (IMC) for the thisulin procursor combined in to fold correctly. The cleavable peptide incher has a C-terminal Arg residue which enables the high portion of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin with an hose protein binderic protein can provide human insulin with or negative protein binderic protein can provide human insulin with correctly linked exercise binders with fewer cheesary procedural stops, and hose resulting in a higher yield of human insulin with sequences from intracellular detachatically processed for intracellular detachatically processed for intracellular detachatically processed for intracellular detachatically processed for the fision protein and decrease the interrolember in the solubility of the fision protein and decrease the interrolember in the
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folding; conformation; chimeric protein; cleavable; recombinant;
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particularly for the production of human insulin
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                                        Claim 14; Page 30-51; 45pp; English.
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This sequence represents a chimeric protein, AGH-mini-proinsuine.

This chimeric protein contains an N-terminal fragment of buman growth horzone (AGH) of the sequence given in AAV42855, a cleavable peptide linker (AAV42857), and a cumman insulin precursor comprising insulin as an intramolecular chapterone (IMC) for the insulin precursor, and intramolecular chapterone (IMC) for the insulin precursor, could correctly. The deavable peptide linker has a clearing it to fold correctly. The cleavable peptide linker has a clearing it to fold correctly. The cleavable peptide linker has a clearing it to fold correctly. The cleavable peptide linker has a clearing that for earnowing the high portion of the cleavable between procedural such National Carpetine of the recombinant human insulin with correctly linked cysteine bridges with lewer necessary procedural steps, and hence resulting in a higher yield to human insulin. The IMC sequences not only protect insulin sequences for human insulin. The IMC sequences not only protect insulin sequences for human insulin precisor, and hence resulting a significant of the figure of the flaced issulin precisor, insulin each promote the figure of the flaced issulin precisor, insulin each promote the figure folding of the flaced issulin precisor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the fusion protein and decrease the intermolecular interactions among the fusion proteins, thus allowing folding of the fused insulin precursor at commercially useful high concentrations. The procedural steps of cyanogen bromide cleavage, oxidative sulphitolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           chimeric proteins containing buman growth hormone fragment, used the large for the production of human insulin .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth hormone, chaperone, intramolecular, insulin, precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       folding, conformation, chimeric protein, cleavable, production, yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.7%; Score 555.5; DB 20;
71.3%; Pred. No. 8e-28;
Live 0; Mismatches 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human growth hormone (ASH) N-terminal fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GFFYIPKTKGIVEQCCISICSLYQLENYON 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEFYTPKTRGIVEOCCISICSLYQLENYCN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                          Claim 13; Page 30; 46pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42856 standard, protein: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-CN00052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-CN03052,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuery Match
Hest Local Similarity 71.39
Watches 107; Conservative
               WPI; 1999-610839/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA;
                                                                                    particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 - JAN - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WC9950302-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-00T-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY42856
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us-09-423-100-7.rag

Weiner RI;

Taylor R,

Struman I,

Martial JA,

WPI: 1999-045192/04.

N-PSDB; AAX01707

(REGC) UNIV CALIFORNIA.

98WO-US09691. 97US-0046394.

12-MAY-1998;

19-NOV-1998.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                  (hGH) which is a component of a chimeric protein (AN42861) which also contains a human insulin precursor (AA42869). The ESH portion of the chimeric protein acts as an intramolecular chaperoue (1MC) for the insulin precursor, enabling it to fold correctly. A cleavable peptide linked with a C-terminal Ang residue (AN42867) enables the huis pertion of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin with an huis-precisation of recombinant human insulin with correctly linked cysteins better protein can provide tuman insulin with correctly linked cysteins better with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin with correctly linked cysteins better with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin and december only protect insulin a sequences from intracellular degladation by a microcramism host, but also protein the folding of the fosed insulin precursor, insuline the solubility of the fusion protein and docrease the interminents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions among the fusion proteins. thus allowing relating of the fused institut precursor at commercially useful high connections. The procedural steps of eyanoges tromide cleavage, oxidative supplitions and related purification steps can thins be eliminated, along with the use of high concentrations of mercaptam or the use of hydrophobic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEPTIPLSRLFONAMIRAGRINGLAFOTYQEFERNIFKEGKYSFLONFQISLSTSFSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saps
                                                                                             New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin ^{\circ}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pre-eclampsia: intrauterine growth retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lough 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              staps:
                                                                                                                                                                        This sequence represents an N-terminal fragment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human anti-angiogenic peptide 16K hsH Met-1Prol33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.0%; Smore 470; 08.20; 100.0%; Pred. No. 1.56-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TPSNREFTQQKSNLELERISLLLIGSWLEPVÇ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismarches
 TONGHUA GANTECH BICTECHNOLOGY LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW92265 standard: Protein: 134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%;
100.0%; Pre
                                                                                                                                         Claim 5; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  placental dysfunction.
                                                               WPI; 1999-510839/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     absorbent resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW92265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
(LONG-)
                                  Gan 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
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This invention describes novel human anti-anglogenic peptides derived from 10 to 150 consecutive amino acids selected from the N-terminal end of from 10 to 150 consecutive amino acids selected from the N-terminal end of human place of human growth hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit of hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit complements in chick thorioaliantoid memorane and (ii) binds to at magingenessis in chick thorioaliantoid memorane and (iii) binds to at magingenessis and chick thorioaliantoid memorane and (iii) binds to at magingenessis and product or high-V. The invention also describes a method for Garnersing a probable abnormality of placental vascularisation during programmy. The peptides can be used for treating an anglogenic disease in a subject, for inhibiting tummour formation or growth in a patient or for modulating vascularisation of a patient.'S placenta. In particular, the peptides can be used for treating or treating as rheumatoid arthritis, athereselerotic plaques, corneal graft neovascularisation, arthritis, andromedial proliferative retinopathy such as theose occurring arthritis, athereselerotic plaques, corneal graft neovascularisation, arthritis, inappropriate vascularisation in wound healing such as hypertrophic sears or keloid sears, neovascular glaucoma, corlar, through such as disorders such as follicular and luteal cysts and choicane, trachoma, vascular adhesions, chronic variant the controcarcinoma, trachoma, vascular adhesions, chronic variant the encoding the peptides can be used as contraceptive agents. DNA cancer in meaning tragments of base of a pacental development associated the absonciated in assays for impairment of vascular development associated by whith pre-celampsia, intranterine growth retardation, and placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti-anglogenic peptides - comprise N-terminal fragments of \operatorname{Numam} placental lactogen, human growth hormone, growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TPSNKEETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TPSNREETOGKSNLELLRISLLLIOSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human growth hormone mutant hPRL (111-129).
                                                                                                                                                              Claim 4: Page 49-50; 87pp; English.
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                                                                                   variant or human prolactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 AA;
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92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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62 PSNREETQOKSNLELLRISLLLJQSWLEPVÇLGTGPRFVNQHLCGS-------H 108

active domain: ETH;

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structure-function relationship; segment substituted polypeption;
mutant; metein.
  Growth hormone, placental lactoment prelacting
            Homo sapters.
Synthetic.
                   US6428954-B1
                                                                  acid
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AAP90129:
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RESULL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The inversion relates to literativing an inknown active densary in the inversion relates to literativing an inknown amino acid sequence in a parent polypeptide or 4 human growth hormone (hGH) which has been cloned and has a pre-identified biological active domain interacts with a target, when the parcit polypeptide is in its native folded form and the interaction is comparant to polypeptide is in its native folded form and the interaction is comparant to a sequence or polypeptide structure in the region of known amino acid sequence or polypeptide structure in a region of known amino acid sequence or polypeptide structure in a region of known amino acid sequence or polypeptide structure in a region of known amino acid sequence or polypeptide contains a region of known amino acid sequence or polypeptide of known amino acid sequence of an analogue of containing at least 15% homology with BGH alpha-carbon coordinates within about 2:55 anguence, where any interaction of the coordinates within about 2:55 anguence, where any interaction of the analogue into DNA encoding the full length hGH, and expressing a sequence consolution of the interaction of the consolution of polypeptide into DNA encoding the full length hGH, and expressing a sequence consolution and polypeptides as an indication of the location of the unknown active domain in hGH. The method is useful for determining the sequences of the relationship between structure and function of the location of the relationship between structure and function of the location of the relationship between structure and function of the location of the relationship between structure and function of the location of match the second assigned to describe and any second sequences. The present sequence is that of hamman growth hormony of the location of the relationship between structure and function of the location of the relationship between structure and function of the location of the relationship between structure and function of the location of the location of the relationsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to identifying an unknown active domain in a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTIPLSRIFONAMIRAHECHQLAFDTYQEFERAY (PREGRYSFLONEGTSLSFSESIF) = 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying active domains within cloned polypeptides of known amino acid sequence by substituting analog segments into the parent polypeptide is useful to determine the relationship between structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The present sequence is not shown in the specification but was created by the indexer using the mature how sequence and information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.0%; Score 470; DB 23; Length 191:
69.2%; Pred. No. 2.6e 22;
tive 8: Mismatches 19; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1: Page -: 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contained in the specification.
                                                                          95US-0483039
                                                                                                                                 89US-0428066
                                                                                                                                                     920S-0875204
920S-0960227
                                                                                                                                                                                                              94US-0190723
88US-0264£11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Bost Local Similarity 69.2
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                     Cunningham BC;
                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-696875/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AA;
                                                                          06-JUN-1995;
                    06-ACG-2002.
                                                                                                                              26-0CT-1983;
                                                                                                                                                          27-APR-1992;
13-OCT-1992;
                                                                                                                                                                                                           02-FEB-1994;
28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                  Wells JA,
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AAW92264

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61 PSWREETQGKSNLEBLER:SELELQSWLEPVQF-LRSVPANSLVYGASDSNVVDILEQLKR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EL TPSNREETOOKSNLELLRISLLLIQSWLEPVQLGTGPRFVNOHLCGS------HLV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1 TPSNREETQQKSNLELLRISLLLIQSWLEPVQF-LRSVFANSLVYGASDSNVYDLLKDLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MFPTIPLSRIFONAMIRAHRIHQLAFDTYQEFEEAYIPKEGKYSFUONPQTSLSFSESIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention consists of a vector contg. a fusion protein which is formed by ligating, downstream of a promoter, hGH or a deriv. (prof. formed by subtstn. or Met.14 with Leu) and a foreign protein. Stability of the vector in the nost is greatly increased so the protein yield is higher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant vector contq. fusion protein – consisting of human growth hormone or deriv. ligated to foreign protein, for stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inde, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human growth hormone; tusion protein; recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.5%; Score 466; DB 10;
70.5%; Pred. No. 4.6e-22;
cive 7; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LVEALYLVCGERGFFYTPKTRGIVEQ 134
                                                                                                                      20 LIEGLMLILSDG --- SPRIGGIFKQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 EALYLVCG--ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                 AAP90129 standard; protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure: Fig 1: 19pp: Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87JP-0304937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87JP-0304937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WAKT ) WAKUNAGA SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 70.5 les 103; Conservative
                                                                                                                                                                                                                                                                                                                                                     (updated)
                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-209284/29.
N-PSDB; AAN90269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and high yield.
                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
06-FBB-1996
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP01144981-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1989.
                  \hat{\Xi}
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Gaps

16;

Indels

20:

Length 192;

; DB 20; 4.6e-22;

Score 466; DB Pred. No. 4.6e 7; Mismatches

58.5%; 70.5%;

Query Match Best Local Similarity 70.5 Matches 103; Conservative

192 AA;

Seguence

Homo sapiens. W09851323-A1 12-MAY-1998; 3-MAY-1997; Martial JA, 98-JUN-1999 dysfunction

Human, anti-angiogenic; prolactin; placental lactogen; hPL; augrogenesis; growth horone; MRH; MRH*V; capillary endotheiaal cell proliferation; placental vascularisation; pregnancy; treatment; angiogenic disease; tumour; inhibitor; maliquan; angiofibroma; arteriovenous malicomation; arthritis; atheroscierotic plaques; corneal grate newscalarisation; wound healing; proliferative retinopathy; macular degeneration; traching granulation; glaucoma; ocular; uveitis; trachare; Csler-Weber syndrome; ulcer; leckaemia; reproductive disorder; contraneptive agent; adhesion; ulcer; leckaemia; reproductive disorder; contraneptive agent; gene therapy; pre-echampsia; intranerine crowth retardation. New anti-anglogenic peptides - comprise N-terminal framents of human placental lactodes, human growth hormone, growth hormone variant or human prolactic Human anti-anglogenic peptide how Met-1Phe191. Woiner RI: Taylor R. AAW92264 standard: Protein; 192 AA. Example 3: Page 49: 87pp; English. 16960SH-0M86 97US-0046394 (first entry) Struman I, (REGC) CNIV CALIFORNIA placental dysfunction. WPI; 1999-645192/04. N-PSDB; AAX01706

111 EALYLVCG - - ERGFFYTPKTRGIVEQ

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This invention describes nevel human anti-angumente peptides nectived from 10 to 150 consecutive amino acids selected from the Negarinal and of human placental lactogen (hE), human trowth hormone (hE), and the bormone variant (hEH-V), or human prolacing such peptides (i) inhibit capillary endethelial cell proliferation and organisation (ii) linhibit anglogenesis in chief cell proliferation and organisation (ii) linhibit anglogenesis in chief cell proliferation and organisation (ii) linhibit anglogenesis in chief cell proliferation and organisation (iii) linhibit and hois, hE, prelation or mSH-V. The invention also discribes a method for diagnosing a probable abnormality of placental vascularisation diring preparacy. The peptides can be used for treation or drowth in a patient or commodilating vascularisation of a pricent's placental in particular, the peptides can be used for treation or drowth in a patient or commodilating vascularisation of a patient's placental in particular, the peptides can be used for preventing or treating each as rheumicid anglofibroma, afteriovenous malformation, arthritic such as rheumicid such as hypertrophic scars or keloid scars, neovascular alaucera, ocular tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis, pyogenic glaucoma, retrolental fibroplasia, scheroderma, solid timnours, Raposi's sarcoma, trachoma, vascular adhesions, chronic varicose micras, leukaemia, and reproductive disorders such as follocular and inteal organ and choriocarcinoma. They can also be used as contraceptive access. DNA abnormal levels of N-terminal fragments of hGH, hGH-V, prolactin of hBL can be used in assays for impairment of vascular development usbodied with pre-columpsia, intrauterine growth retardation, and placental arthritis, atherosclerotic plaques, corneal graft necessoriarisation, delayed wound healing, proliferative retinopathy such as diametic retinopathy, macular degeneration, granulations such as those occurring in hacmophilic joints, inappropriate vascularisation in wound healing

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    duman growth hormone segment, used at the N-terminal of a fusion protein, which contains a thrombin recognition site, and human beta nerve growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the folsion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91299).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEPTIPLSHIFDNAMIRAHRLHQIAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w human nerve growth factor gene encoding lusion protein having cleavage site for thrombin, useful for treating geriattic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 140;
                                                                                                                                                                                              geriatric dementia; nervous disorders; human nerve factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 465; DB 10; 98.9%; Pred. No. 4.2e-22;
                                                                                                                                                                                Human growth hormone; fusion protein; thrombin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGIQTLMGRLEDG---SPRIGGIFFQ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; page 21; 38pp; English.
                                                                         AAP9104: standard; protein; 340 AA
                                                                                                                                                        Human growth hormone segment,
                                                                                                                                                                                                                                                                                                      89EP-6102795.
                                                                                                                                                                                                                                                                                                                                 88JP-0035042.
                                                                                                                             (first entry).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Conservative
                                                                                                                                                                                                                         Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-243092/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AA;
                                                                                                                                                                                                                                                                                                                                                           HOSOL ( LAGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dementia, etc.
                                                                                                                                                                                                                                                                                                      17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                 19-FEB-1968;
                                                                                                                             14 - DEC - 1989
                                                                                                                                                                                                                                                 SP329175-A.
                                                                                                                                                                                                                                                                            23-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                    htsuka E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                  AAP91041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                               S LIGSEY
                                                           AAP91041
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RESULT 9 AAP91299

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1 MEPTIFLSRLFDNAMLRAHKLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purifich. Of human neuron growth factor beta-subunit-courg, protein by contacting with get having eation exchange gp. in presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be produced as this fusion protein. It is purified by contacting a gel maying a cation exchange gp. with the fusion protein, in the presence of urea. The purified protein is useful in a medicament is in realing disorders of the nervous system, eq dementia. (Updated on 25-WAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A recombinant human nerve growth factor beta subunit-contg, protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-cell stimulatory factor-2, interleukin-6, B-ceil difforentiation,
Enterleckin-5, fusion protein.
                                                          Human growth hormone/human nerve growth factor beta fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B-ceil stimulatory factor-2 and B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 465; DB 12;
Pred. No. 6.8e-22;
                                                                                                                 hOH; hNGF; nervous system diseases; dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TPSNRESTQQKSNLSTLRISTLIOSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TPSNREETQCKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.smatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure ; fig 1; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AARC3255 standard; protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.38;
98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88JP-0162556.
                                                                                                                                                                                                                                                                                                                                        89JP-02028 35
                                                                                                                                                                                                                                                                                                                                                                                               69JP-0202835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88JP-0162556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (tirst entry)
  25-JUN-1991 (Elist entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.9
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WP1: 1991-128768/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOYL) TUSON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fision protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ11578.
                                                                                                                                                                                                                                                                                                                                                                                               27 - AUG - 1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JPC2013375-A.
                                                                                                                                                                                                                         JP03067598-A.
                                                                                                                                                                                                                                                                                                                                        77-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51-JUL-1988;
                                                                                                                                                                        Home sapreds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-JUL-1990
                                                                                                                                                                                                                                                                                 22-MAR-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR33255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminal end (1st region), a 3 amino acid sequence representina thrombin recognition site, and buran beta nerve drowth factor (beta-NUF) at the C-terminal. Beta-NUF can be used to control geriatize demotia and other nervous disorders, and can be released from the lusion protein by incubation with thrombin (see AAN96577-9, AAP91034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEPTIPOSHUPDNAMIRAH PUNGLAPDINGEPBATTEKBONNSHONPOTSIJSPISES (R. f. ...) | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human nerve growth factor gene encoding fusion protein - having cleavage site for thrombin, useful for treating geriatric
                                                                                                                                                                                                                                                                                                           Human nerve growth factor and human growth normone fusion protoff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 465, 18 10; Length 261;
Pred. No. 6.8e-22;
0; Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                               Human nerve growth factor; Bugion protein: thrombing geriatric dementia; nervous disorders; human growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pusion protein consisting of human growth hormone at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THISTITI FILL FILL FILL CHILLOSMEEPVO 92
61 TPSNREBTQQKSNLELLR.SLLLLTQSWLEPVQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPSNREETQOKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1.140
141.143
144.261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 36; page 31-32; 38pp; English
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                                                                                                                                        AAP91299 standard: protein; 261
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98.9%;
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                                                                                                                                                                                                                                                         (first entry)
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Matches 91: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dementia, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Home sapiens
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                                                                                                                                                                                                                                                       14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP329175-A.
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Region
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RESULT 10

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Claim 10; Page -; 74pp; English.
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92JS-0875204.
92US-0960227.
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88US-0264611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-950-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wells JA, Cunningham BC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                        191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant: mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1992;
13-OCT-1992;
02-FEB-1994;
28-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6428954-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                         Segmence
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG94860;
                                                                                                                                                                       hormone
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        ABG44860
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                                                                                                                                                                                                                                           t i
                                                                                                                The protein is produced by fusing DNA encoding 3DF (II.-) with DNA encoding BSF-2 (IL-5)and ligating the product into an expression vector See also AAR05311 and AAR05113.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human, growth hormono: hGH; Turner's syndrome; schoudrop)asta: growth hormone deficiency in adults; GHDA: chronic renal insultationery renal failure in children; acquired incume deficiency syndrome; AIDS: AIDS wasting; cachexia: mutsat, purcie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New conjugates exhibiting growth hormone activity, useful for treating a disease or for manufacturing a medicament for treating a disease, e.g. Turner's syndrome, growth hormone deficiency, achondropiasia, AIDS wasting or cachexia
                                                                                                                                                                                                                                 1 MEPTIPLSRLFONAMLRAFRLHQLAPOTYQEFEEAZIPKEGKYSFLQNPQTSLSFSFSIF
                                                                                                                                                                                                     Gaps
                                                 Preps. of human B-cell differentiation factor - from specified bux sequence segment, by recombinant DNA technique, gives protein of specified amino acid sequence.
                                                                                                                                                                            58.3%: Score 465; DB 11: Length 810; 98.9%; Pred. No. 7.26-22; Live 0; Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "Wild type And substituted by Lys"
                                                                                                                                                                                                                                                                          61 TPSKREETQQKSNLEDLRIGGSWLEPVQ 92
                                                                                                                                                                                                                                                               61 TPSNREETOOKSNLELLRISLLJIQSWLEPV0 92
                                                                                                                                                                                                                                                                                                                                                                                                    Mature human growth hormone (hGH), mutant #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen KV, Drustrup J, Christiansen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualitiers
                                                                                            Claim 31; Page 9; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                      ABG31862 standard; Protein: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAXY-) MAXYGEN HOLDINGS LIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2001; 2001DK-0000042.
11-JAN-2001; 2001US-261411P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2002; 2002WO-DK00017.
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                   Conservative
                    WPI; 1990-062207/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MAXY-) MAXYGEN APS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 134
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 91; Conserv
(TOYS ) TOSOH CORP.
                                                                                                                                                           Sequence 310 AA
                               N-PSDB; AA002028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200255532-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2032
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                                                                                                                                                                                                                                                                                                                                                          ABG31862;
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(GE) activity and comprise at least one non-polypeptide group covalently attached to a GE polypeptide. The amino acid sequence of the conjugates differs from that of wild type human GH in at least one introduced and at least one removed amino acid residue comprising an attachment group for the first non-polypeptide group. The conjugate or pharmaceutical medicament for treating a disease or for manufacturing a medicament for treating a disease or for manufacturing a medicament for treating a disease, e.g. Turner's syndrome. GH deficiency in adults (i.e. GHDA), achonicroplasia, chronic renal insufficiency of failure (including renal failure in children), acquired immune deficiency syndrome (AIDS) was ting, cachexia in AIDS patients, or cachexia associated with other diseases. The conjugates are useful for treating a variety of disorders caused by growth hormone inadequacy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6. PSNREETQOKSNLELLESELLIGSWLEPVQF-LRSVFANSLVYGASUSNVYDLLKDLEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PSNREETQQKSNLHILLISLLLIQSWLEPVQLGTGPRFVNQHLCGS------HLVE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not shown in the specification but is derived from the wild type human growth hormone sequence given in SEQ ID No.2 (see ABG31957).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | FPT1PLSELFDNAM.RAHREHQLAFDTYQEFERAYIPKEQKYSFLQNPQTSLCFSESIPT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSFSIPT 61
The invention relates to new conjugates, which exhibit growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth hormone, placental lactogen, prolactin, active domain, hGH, structure-function relationship; segment-substituted polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 58.2%; Score 464; DB 23; Length 191; Local Similarity 71.6%; Pred. No. 6.1e-22; es 103; Conservative 6; Mismatches 20; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human growth hormone mutant hPD (109-112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ALYLVOG -- ERGFFYTPKTRGIVEG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GIQTLMGRLEDG---SPKTGQIFKQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
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The invention relates to identifying an extrost active demain in a region of known amino acid sequence in a parent polymentage of the active has been cloned and has a pre-identified thost lives of carivity, where the active cloned and has a pre-identified thost lives the active domain interacts with a turge when the partial polymentage is in its native-folded form and the interaction is responsible for the holospical activity exprision; of comparing the amino acid sequence of polymentage of high with the artino acid sequence of high with the artino acid sequence of an analogue production of known amino acid sequence of an analogue operation of known amino acid sequence of an analogue operation of known amino acid sequence of an analogue operation of known amino acid sequence or polymentage of an analogue action of known amino acid sequence or polymentage of the acid of the acid of a consideration of the acid of a consideration of the acid of a consideration of the acid of acid of a consideration of the acid of acid of a consideration of the consideration of the acid of a consideration of the cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e) comparing the difference between activity of the first and second segment-substituted polypeptides as an indication of the location of the unknown active domain in AGH. The method is useful for determining
                                                                                                        acid sequence by substituting analog sequents into the parent, polypeptide is useful to determine the relationship between structure
                                                                        identifying active domains within closed polypoptides of known artho-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The present sequence is not shown in the specification but was created by the indexer using the mature NGH sequence and information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the relationship between structure and function of known polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences. The present sequence is that of human growth hormobic mutant substituted with resilues from an holf analogue (prolacin) placental lactogen or porcine growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and (c) with a second analogous polypeptide segment, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ADYLVCG - - ERGFFYTPKTRG1VEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GLOTLMGRIEDG---SPRTGGIFKQ :41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG94977 standard: Protein; 191 AA.
                                                                                                                                                                                                                                    skample 1; Page -; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contained in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
WPI: 2002-696875/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG94977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (a) (e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG94977
      q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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control of the sequence in a parent, polypeptide e.g. thuman growth cormone (hGH) which has been cloned and has a pre-identified biological activity, where the active domain interacts with a trarget when the parent polypeptide is in its native-folded form and the interaction is responsible for the biological activity comprising: (a) comparing the amino acid sequence of polypeptide structure in the region of known amino acid sequence of polypeptide structure in the region of known amino acid sequence of polypeptide structure in the region of known amino acid sequence or polypeptide structure in the region of known amino acid sequence or polypeptide (e.g. prolactin, placental lactogen or porcine growth normone) which has at least 15% homology with hGH alpha-carbon coordinates for about 60% of the analogue sequence, where any interaction of the analogue with the target is different from tranget interaction of the analogue into DNA encoding the full length hGH, and expressing a malogue into DNA encoding the full length hGH, and expressing from the conjugation of the different contaction; (b) substituted polypeptide; (c) contacting the sequent; and second analogues polypeptide sequent; and second analogues polypeptide.

segment-substituted polypoptides as an indication of the location of the unknown active domain in hGH. The method is useful for determining the relationship between structure and function of known polypoptide sequences. The present sequence is that of human growth hormone mutant substituted at functionally important residues and used in

The present sequence is not shown in the specification but was d by the indexes using the mature HGH sequence and information

contained in the specification.

created by the

191 AA;

Sednence

the method of the invention.

The invention relates to identifying an unknown active domain in a region

Example 16: Page -; 86pp; English.

and function

anid sequence by substituting analog segments into the parent polypoptide is useful to determine the relationship between structure

Identitying active domains within cloned polypeptides of knows amino

920S-0875204. 920S-0960227. 940S-0190723. 880S-0264611.

27 - APR-1992; 13 - OCT-1992; 26-0CT-1989:

28 - CCT - 1989

02-FEB-1994

Wells JA, Cunningham (CETH) GENENTECH INC

WPI: 2002-696875/75.

95US 0483039. 8905-0426056

06 - JUN-1995;

US6428954-BI

Synthetic.

06 - AUG - 2002

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Ö
                                                                                                                                                                                                                               61 PSWREETQGKSNLEELRIS LELOSMLEPVQF-ERSVFANSLYYGASOSODYHILKDLEE 119
                                                                                                                                                                                                  62 PSUREETQOKSULHLGRIS LLIQSWLEPVQLGTGPRFVNQHLGGS-----HLV---E 11]
                                                                                                                                   2 FPTIPLSRLFDNAMLRAHRIHOLAFDTYOFFEBAYIPKBOKYSFLONPOTSLSFSESIPT 61
                                                       16; Gaps
58.1%; Score 453; DB 23; Length 191: 71.0%; Pred. No. 7.1e-22;
                                                       indels
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Growth hormone; placental lactoges, prefacting active density, hossistructure-function relationship; segment-substituted polypeptide:
                                                                  Human growth hormone mutant 7163A.
                                            03-DEC-2002 (first entry)
                                                                                                                  mutant; mutein.
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Homo sapiens.

62 PSNREETQQKSNLFLLRISHLIQSWLEPVQLGTGPRFVNQHLCGS------HLVE 111 PSNREETUCKSNLELLRISLLLIQSWLEPVQF-LRSVFANSLVAGASDSNVYDLLKDLEE 119 60 61 2 FPTIPLSKLFUNAMLKAHKLHQLAFDTYQEFEBAYIPKEQKYSFLQNPQTSLSFSESIPT 16; Caps 58.1%: Score 463; DB 23; Length 191; 76.3%; Pred. No. 7.1e-22; ive 7; Mismatches 20; Indels 16 Pred. Nc. /... 7: Mismatches 112 ALYLVCG--ERGFFYTPKTRGIVEQ 134 -: -: Conservative Sest Local Similarity Matches 102; Conserv prery Match 8 ð ŝ 3

120 GIQTLMGKLEDG---SPRTGQIFKQ 141

a

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The sequence encoding this protess can be tused with DNA encoding Breell differentiation factor (IL-6) and ligated into an expression vector to prodm. of a fusion protein. See also AAR05311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preph. of human Breell differentiation factor - from specified DNA sequence segment, by recombinant DNA technique, gives protein of specified asino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oucry Match 58.0%, Score 462, 18 11, Lougth 144: Best Local Similarity 97.8%; Pred. No. 6.66-22; Matches 90; Conservative 1, Mismatches 1: Indels
                                                                                            Segment of Breell Stimulatory factor-2 (12.5).
                                                                                                                    B-cell stimulatory factor-2: interleukin-5.
                       AAR05313 standard: protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 9: 17pp; Japanese.
                                                                                                                                                                                                                 88.32-0162556
                                                                                                                                                                                                                                       83JP-0162556
                                                                      19-JUL-1990 (first entry)
                                                                                                                                                                                                                                                                                   WPI; 1990-062207/09.
N-PSDB: AAQ02028.
                                                                                                                                                                                                                                                               (TOYU ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14: AA:
                                                                                                                                                                                                                                       01-JUL-1988;
                                                                                                                                                                  JP02013375-A.
                                                                                                                                                                                                                01-JUL-1988;
                                                                                                                                             Homo sapiers
                                                                                                                                                                                         17-JAN-1990.
                                                AAR05313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
RESULT 15
AAR05313
ID AAR051
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60

Search completed: September 16, 2003, 12:38:27 Job time: 45.358 secs

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NAME: Johnston, Scan A. REGISTRATION NUMBER: P35,910
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
                     Sequence 1, Appliance 2, Appliance 3, Appliance 16, Appliance 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Appl. Sequence 4, Appl. Sequence 4, Appl. Sequence 4, Appl.
                                                                                                          September 15, 2003, 12:37:10 / Search time 23:53 Seconds (without disamments) 255:217 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10. A Sequence 10. A Sequence 10. A Sequence 11. A Sequence 11.
                                                                                                                                                                                                                            1 MEPTIPLSRLFDNAMIRABE................TVEQCCTSICSLYGLENYCN 150
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCare version 5.1.6 Copyright (c) 1993 - 2003 Compuser Ltd.
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0.8-04-384-871-4

0.8-08-384-621-4

0.8-08-784-582-1

0.8-08-784-878-1

0.9-28-784-878-1

0.9-28-784-878-1

0.9-28-03-6-8

0.9-28-878-1

0.9-28-03-6-8

0.9-28-03-6-8

0.9-28-03-6-8

0.9-38-78-6-1

0.9-42-9

0.9-420-819-36-1

0.9-420-819-36-1

0.8-09-420-819-36-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-18-093-383-1
                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 10%
Maximum Match 100%
Disting first 45 symmaties
                                                                            - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match
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57.1
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56.2
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45.9
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Perfect score:
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                                                                            OM protein
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                                                                                                                                                                                                                               Sequence:
                                                                                                                 Run on:
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              Parent No. 5424199
Sequence 5, Appli
                                       Sequence 5, A
Sequence 5, A
Sequence 5, A
Sequence 8, A
Sequence 39, B
Sequence 48, A
                                                                                                                                                                                                      Sequence 4, 7
Sequence 6, 7
Sequence 2, 7
                                                                                                                                                                                                                                                                                                         RESULT 1
US-10 093-183-1
Sequence 1, Application US/08093183
Sevence 1, Application US/08093183
CENERAL INFORMATION:
APPLICANT: Devect, Herman A.
APPLICANT: Beyneker, Herman A.
APPLICANT: Perfect H.
TITLE OF INVENTION: One of Sevine Growth Hormone NUMSER OF SECTENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                           Sequence 8
Sequence 1
5424.99-3
5424.99-3
08-08-710-3248-5
08-08-110-3248-5
08-08-180-3768-5
08-08-160-3768-5
08-08-160-3768-5
08-08-10-356-39
08-08-400-256-39
08-08-400-256-39
08-08-400-256-48
08-08-400-256-48
08-08-400-256-48
08-08-400-256-48
08-08-400-256-48
08-08-400-256-48
08-08-406-58-48
08-08-406-58-48
08-08-406-58-48
08-08-406-58-48
08-08-468-824-8
08-08-160-38-468-82-45
08-08-160-38-468-82-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REMOMBLE FORM:
MEDIUM TYPE: 5.25 inch. 366 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ACLUOSAMELUGS
                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: C. DONAMS-LOSS SOFTWARE: DATE: (C.DOLOGILECH)
CURRENT APPLICATION DATA: ASPLICATION DATA: US.CB./093,385
EILING TATE: 14-707-1993
CLASSIFICATION TOWNER: US.CB./093,385
FRICR APPLICATION GAR:
APPLICATION WIMBER: C7/19824
FILING DATE: 28-NOW-1990
PRIOR APPLICATION WIMBER: C7/19824
FILING DATE: 05-APR-1988
FROM APPLICATION NUMBER: G6/63261
FRICH APPLICATION NUMBER: G6/63261
FRICH APPLICATION NUMBER: G6/63261
FRICH APPLICATION DATA:
APPLICATION NUMBER: G6/63261
FRICH APPLICATION DATA:
APPLICATION WIMBER: G6/63267
FILING DATE: 19-JUL-1984
APPLICATION WIMBER: G6/36367
FILING CATE: 18-SEP-1901
ATICRNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ...ormESEE: Genericch, Inc.
STREET: 460 Foint San Bruno Blvd
CITY: South San Francisco
STATE: California
CCONTRY: CSA
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2 FPTIPLSRIFDNAMIRAHRIHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESTPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 FPTIPLSKLFSNAMLRAHRLHQLAFDIYQEFBEAYIPKEOKYSFLQNPQTSLCFSESIPT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Stabilization of Somatotropins and Other TITLE OF INVENTION: Proteins by Modification of Cysteine Residues NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LHW PC compatible
CREMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%; Score 461; DB 2: 76.3%; Pred. No. 3.8e-42; tive 7; Mismatches 20,
                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Estelle J. Tsevdos
STREGT: 1937 West Main Street, P.O. Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.,278-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 07/766,142
FILMG DATE: 25-SEP-1991
APPORREY/AGENT INFORMATION:
NAKE: ISSUGDE: 21-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL: INFORMATION:
APPLICANT: Daley, Michael J.
APPLICANT: Cady, Susan M.
APPLICANT: Cady, Susan M.
APPLICANT: Shieh, Hong Ming
APPLICANT: Shieh, Hong Ming
APPLICANT: Seddon, Acdrew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4. Application US/08459906
Parent No. 6010999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NOWHER: 31
THIRCOMMUNICATION INFORMATION:
FELEPHONE: 203-321-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 203-710-474-4059
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 amine acids amine acids
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APPLICATION NUMBER: US.
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Matches 102; Comservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 203-422
TTT FPAX: 263-321-2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCLEGULE TYPE: protein
                                                                                                                                                                                                                                              STATE: Connecticut
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
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                                                                                                                                                                                                                                                                                                   RY: U.S.A.
06904-0060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 36
CLASSIFICATION:
                                                                                                                                                                                              Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Wayne
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                                                                                                                                                                                                                                                                                                   CCUNTRY:
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US-08-459-906-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jazaran, Martha Guerrero
APPLICANT: Saldana, Esco Pariera
APPLICANT: Saldana, Esco Pariera
APPLICANT: Saldana, Esco Pariera
IIILE DE INVENTION: Genetically Modified Methylotrophic F. pastotus Yests:
IIILE DE INVENTION: Genetically Modified Methylotrophic F. pastotus Yords:
IIILE DE INVENTION: Production and Secretion of the Human Growth Hormone FILE REPERBORE: 1829,0010000
CURRENT APPLICATION NUMBER: 1920-67-21
PRIOR PAPLICATION NUMBER: POT/MX97/C0033
PRIOR FILING DATE: 1937-10-24
                                                                                                                                                                                                                                                                                                                                                                                            | FILLSOFIED | FILE | F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | THIST | THISTITH FOR THE CONTROL OF THE CONTROL O
                                                                                                                                                                                                                                                                                                                                        1 MEPTIPLSRIEDNAMLRABRLEQUAFDIYOHEERYTEKEGRYSELGNEGTSLSFSESIE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels 16; Saps
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APPLICANT: Buckwalter, Hrian I.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Shieh, Hong-Ming
APPLICANT: Boblen, Peter
APPLICANT: Seddon, Andrew P.
APPLICANT: Seddon, 
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                                                                                                                                              Longth 1920
                                                                                                                                    58.5%; Score 466; DB 1; Bength 19170.5%; Pred. No. 1.16-42; Live 7; Mismatches 20; Indols
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Pred. No. 3.7e-42;
7; Mismatches 20
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Patent No. 6342375
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/ Patent No. 5951972
/ GENERAL INFORMATION:
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                                                                                                                                    Query Match
Best Local Similarity 70.5%
Matches 103; Consorvative
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Best Local Similarity 76.3#
Matches 102; Conservative
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ORGANISM: Homo sapiens
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                               US-08-093-383-1
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SEQ ID NO 5
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57.8%; Score 461; DB 3; Lengt; 217; 76.3%; Pred. No. 4.4e-42; Live 7; Mismatches 20; Indels
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                 NAME: Highlander, Steven D. Steven D. Steven D. Statschafton NUNBER: 47,642 REFERENCE/DOCKET NUMBER: UISD:426\HYLTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halban, Philippe A.
No. 6116707mington, Karl D.
Clark, Samuel A.
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PILING DATE: 15-OCT-1996
PRIOR APPLICATION DATE: US 08/589,028
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 ALYLVCG--ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 GIQTLMGRLEDG---SPRTGOIFKO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/784,582
FILING DATE: Concurrently Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Phillippe A. APPLICANT: No. 6116797mington, Kar. APPLICANT: Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-68-784-562-10
Sequence 10, Application US/08784562
Fatent No. 6110707
                                                                                                 HALEPHONE: (512) 418-3600
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thigpen, Anice E. AFFLICANT: Quaade, Christian AFFLICANT: Kruse, Fred
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     : 217 amino acids
amino acid
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Best Local Similarity 70.33
Matches 102; Conservative
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US-08-589-028-10
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APPLICANT: Halban, Philippe
APPLICANT: Halban, Philippe
APPLICANT: Clark, Samidron, Karl D.
APPLICANT: Clark, Samidron, Karl D.
APPLICANT: Thiqpen, Ance F.
APPLICANT: Thiqpen, Ance F.
APPLICANT: Wruse, Fred
TILLE OF INVENTION: Secretory Cell Linus
CORRESPONDENCES: 50
CORRESPONDENCES ADDRESS:
ADDRESSEE: Arcold, White & Durkee
STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indels 16;
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                                                COMPUTER: JBM PC computible
OPERALING SYSTEM: PC-POS./KS-DCS
SOFTWARE: Patentin Release 41.0, Version 41.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/CB/459,906
FILING DATE: OS-JUN-1995
CLASSIFICATION: 514
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,028
FILING DATE: Concurrently Herewith
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Patent No. 6097129
GENERAL INFORMATION:
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Webster, Darryl L.
REGISTRATION NUMBER: 34,276
REFRENCE/DOCKET NUMBER: 31,27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3247
TELERAX: 201-831-3305
                                 Floppy disk
                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-831-3305
INFORMATION FOR SEC ID NO: 4
SEQUENCE CHARACIERISTICS:
LENGTH: 194 amino acids
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 70.33
Matches 102; Conservative
           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-08-589-028-10
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  Gaps
20; indeis 16;
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TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE: 79
CORRESPONDENCE ADDRESS:
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94..115
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                      STRANDEDNESS
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LOCATION:
FEAIURE:
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                                          : TOPOLOGY:
TS-68:785-271-10
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US-08-759-628-11
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                                                                                                                                                                                                                                                                           235 Indeis 16, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECHETCRY CELL LINES
NUMBER OF SECTENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  57:8%; Score 461; DB v; Length 217; 76:3%; Pred. No. 4:4e-42; Live 7; Mismatches 20; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release *1.0, Version *1.30 COURENT APPLICATION DATA: 05/06/2785.271 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Philippe A.
APPLICANT: No. 619476mington, Karl D.
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Quaade, Christian
APPLICANT: Kruse, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 ALYLVCG - ERGFFYTPKIRGIVEG 134
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FRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/569,028
FILING DATE: 19-CAN-1996
AITONNEY AGENT: UPORRATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSRE: Arnold, White & Durkee SIREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UTSD:513
UTSD:514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 37,642
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                   TELEFAX: $12/474-7577
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 512/474-7577
INFORMATION FOR SEG ID NO: 10:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER:
                                      512/418-3000
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.3%
Matches 102: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                       STRANDEDNESS
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                                                                                                                                                                                             US-08-784-582-10
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                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY
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                                                                                                                        Gaps
57.8%; Score 461; DB 3; Length 217;
70.3%; Pred. No. 4.4e-42;
Live 7; Mismatches 20; Indels 16;
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APPLICANT: Alimann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMALIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 ALYLVGG--ERGFFYTPKIRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROGRAPHICATION 473.
PROGRAPHICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,699
REFERENCE/DOCKET NUMBER: DX05520
TELECHANKI A15-496-1200
TELEPHONE: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 GIOTIMGRIEDG --- SPRTGGIFKG 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08759628
Patent No. 6225446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
Query Match
Bost Local Similarity 70.33
Matches 102; Conservative
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32..53
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TITLE OF INVENTION: Process for proparing recombinant proteins using highing to a substance of ficient expression vector from Sacharomyces cevevision
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APPLICANT: Hiqashikuni. Nachiko

APPLICANT: Hiqashikuni. Nachiko

APPLICANT: Hiqashikuni. Nachiko

APPLICANT: Hiqashikuni. Nachiko

APPLICANT: Kondo, Masaaki

APPLICANT: Kondo, Masaaki

APPLICANT: Kondo, Masaaki

APPLICANT: Nachiko BNPEPARING USEFUI. POLYPEPTIDES THROUGH EXPRESSION OF THE

ITLE OF INVENTION: DNAS

FILE REPERENCE: 82.1026

CURRENT PILING DATE: 1999-03-26

CURRENT PILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: 2710-87339/1998

EARLIER FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 66

LENGTH: 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (11 PSWREETQQKSWLELLRISILLIQSWLEPVQF-LRSVFANSLVYGASDSWYDLKDLEE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FPTIPLSKLFDNAMUKAHRLHOLAFDTYOEFFEAYIPKEQKYSFLQNPOTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 241;
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Overy Match 57.8%; Score 461; D8 4; Length 24 Best Local Similarity 70.3%; Pred. No. 5e-42; Matches 102; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BACHMAN & LAPCINTE, P.C.
STREET: Suite 1201, 900 Chapel Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/424,620B
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM OPERATING SYSTEM: WINDOWS 95/98 SOFTWARE: MS WORD CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SFO ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 ALYLVGG -- ERGFFYTPKTRGIVEQ 134
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. Sequence 66. Application US/09280030A
. Patent No. 6506595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 241 amino acids TYPE: amino acid
                    BAE, Cheon-Scon
                                                                                      SEONG, Baik-Lin
MCKON, Jae-Woong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                         YANG, DoorSuk
LEE, JeerWon
                                                                                                                                                                                                                                    CITY: New Haven
STATE: Connecticut
                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                               62 PSNREETQOKSNLELLRISLLLIQSWLEPVOLGTGPRFVNQHLCGS-------HIVE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 FPTIPLSRLEDNAMLRAHRLEGLAFOTYQEFEEAXIPKEQKYSFLQNPQTSLCESESIPT 86
                                                                                                                                                                                                                                                                               2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQFFEEAYTPKEQKYSFLQNFQTSLSFSFSTPT 61
                                                                                                                                                                                                                                      16; Gaps
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                                                                                                                                                                                           Score 461, DB 3; Length 217;
Prod. No. 4.46-42;
7; Mismatches 20; Indels
                                                                                                    /potew "The peptides above and depicted in Figure 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 GIQTLMGRLEDG---SPRTGQIFKO 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1. Application US/69284978
Patent No. 6342375
GENERAL INFORMATION:
APPLICANT: Diazaran, Martha Guerre
                                                                                                                                                                                           57.8%;
70.3%;
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Matches 102, Conservative
                                                                                                                                                                                                                                      Matches 102; Conservative
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PRIOR FILLING DATE: 1997-1
NUMBER OF SEQ ID NOS: 9
                                                             NAME/KEY: Peptido
LOCATION: 192.,210
CTHER INFORMATION: /
OTHER INFORMATION: d
Peptide
143...154
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Best Local Similarity
                      LOCATION:
NAME/KEY:
                                                                                                                                                    US-08-759-628-11
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Ouery Match
Best Local Similarity
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                                                                                                                                                                              56: 3aps
OTHER INFORMATION: Description of Artificial Seguence: Designated a OTHER INFORMATION: an amino acid sequence of MWDsp-MWDp20-IEV-0-GH
                                                                                                                                                                                                                                                             62 PSNREETQOKSNLELLHIGSWLEPVQLGTGFFVNUHLGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Quaade, Christian
APPLICANT: Kruse, Fred
APPLICANT: MCGATTY, Denis
TILLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETCRY CFIL LINES
CORRESPONDENCE: 79
CORRESPONDENCE ADDRESS:
                                                                                        Query Match 57.8%; Score 461; E8 4; Londih 245; Best Local Similarity 70.3%; Pred. No. 5.2e-42; Matches 102; Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDICM TYPE: Floppy disk
COMBUTER: IBM PC compatible
COMBUTER: IBM PC compatible
COPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RCHEASE F1.0, Version #1.33
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/784,562
FILING DATE: CONCULTANTLY Rerewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Newgard, Christopher B.
APPLICANT: Halban, Philippe A.
APPLICANT: No. 6110707mington, Karl D.
APPLICANT: Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CONCULTONILY REFEWITE CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-00r-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 03/589,028
FILING DATE: 19-CAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    112 ALYLVCS - ERGFFYTPKIRGIVED 134
                                                                                                                                                                                                                                                                                                                                                                                   174 GIQTLMGRLEDG---SPRIGGIFKQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s: Arrold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UTSD: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 71, Application US/06/94582 Patent No. 5110707 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37,642
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INFORMATION FOR SEU TD NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDICH TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-784-582-71
                                             US-09-280-030-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY
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62 PSNREETQQKSNLELIRISLILIQSWLEPVQLGTGPRFVNQHLCGS------HLVE 111
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                                                                                                                                                                                                                                        Caps
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NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                        16;
57.8%; Score 461; DB 3; Length 274; 70.3%; Pred. No. 6e-42; ive. 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
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Pred. No. 8.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 ALYLVCG - - ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 SIQTLMGRLEDG---SPRIGGIFKQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-784-592-73
Sequence 73, Application US/08784582
Parten: No. 6.16707
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 73;
SECUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.8%; 70.3%;
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                                                                                               Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSER: Arnold, Whi
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
    Query Match
Best Local Similarity
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62 PSNREETQQKSNLELLRISILLIQSWI,EPVQLGTGPRFVNQHLCGS------HLVE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 455; DB 1; Length 217; Pred. No. 2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FERRARY, GREGORY D.
RECTSITRATION NUMBER: 36.134
REFERENCE/DOCKET NUMHER: 325800-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1760
TELEPHONE: 201-994-1760
TELEPHONE: 201-994-1760
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ALYEVCG - - ERGFFYTPKTRGIVEG 134
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/187,756C
FILLNG DATE: January 27, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 217 AMINO ACIDS
AMINO ACID
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Best Local Similarity 69.77
Matches 181; Conservative
                                                                                                                                                                                                                      PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLCGY: LINEAR MOLECULE TYPE: PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-187-756C-4
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Fatent No. 634844
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: GLOAD STOWTH HORMONE tO STIMULATE hematopolesis and immune reconstitute OF INVENTION: after hematopoletic stem cell transplantation in humans:
TILLE OF INVENTION: after hematopoletic stem cell transplantation in humans:
FILE REFERENCE: CRAPPEL-6.1
CURRENT APPLICATION NUMBER: 05/09/465,461
CURRENT APPLICATION NUMBER: 65/112.668
PRIOR APPLICATION NUMBER: 65/112.668
PRIOR FILING DATE: 1998-12-7
NUMBERS OF SEC. 12 NOS: 1
SECHWARE: Patentin version 3.1
SECHWARE: Patentin version 3.1
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                                                                                                             2 PPTPDSRLFONAMIRAHRIHQLAPDTYQBEERAYITKBOXYBFLONPUTSLSTSESIT 61
                                                                                                                                                                  27 PPTIDESRLEDWAMLRABRIEGLAFOTYOGFERAYIFKROWSFLOWEGTSL/FSESTET ++
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69.78; Pred. No. 1.7e-41;
tive 7; Mismatches 25; indels :
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     7; M.Smatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ROSEN, ET AL.
TITLE CF INVENTION: SHEAL GROWTH SEZMONE
CORRESPONDENCE ALDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GIQTEMGREEDG --- SPRUGGIFKG 141
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4. Application US/08187756C Patent No. 5597709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6 BECKER FARM RGAD
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     102; Conservative
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STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
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CRGANISM: homo sapiens
US-09-465-461-1
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Matches
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OM protein - protein scarch, using sw model

September 16, 2003, 12:38:55; Search tire 47:2753 seronds (without alianments) 472:415 Million ceil updates/ser Run on:

US-09-423-100-7 Title: Perfect score:

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556259 seqs, 148393369 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2600063060

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/ cgn2_6/ptodata/2/pubpaa/USO7_pUBCONE.pcp...
/ cgn2_6/ptodata/2/pubpaa/USO7_pUBCONE.pcp...
/ cgn2_6/ptodata/2/pubpaa/USO6_bENE_cop...
/ cgn2_6/ptodata/2/pubpaa/USO6_pUSCONE.pcp...
/ cgn2_6/ptodata/2/pubpaa/USO6_pUSCONE.pcp...
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/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCONE.pcp...

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/cgn2_6/pt.odata/2/pubpaa/056--_NEW_PUB-pop.+ /cgn2_6/pt.odata/2/pubpad/056--_0000000-pop.+

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the posult being printed; and is derived by analysis of the total score distribution.

Description	Seq verse 7. And 1		Settlement A Settlement	, e	Sequence 1. April 1				Sognence 6, Apply	٠.			Secuence 4. App.	Sequence 16, Appl	Sequence 4, Appli
ID	US-10-054 873-7	CS-10-054-873-6	1 05-70-054-833-2	1 08-09-984-010-23	2 US-16-153-207-1	2 US-10-403-377-1	2 08-10-400-708-1	2 US-10-238-148-1	2 US-10-153-207-6	US-09-929-918-9	US-09-280-032-66	US-09-853-688-2	US-09-969-1480-4	US-09-804-409A-16	US-09-853-688-4
å Query Match Length DB	150 14	107 14	92 14	191 11	191	191 12	191	191 12	214 :2	217 9	245 9	217 9	217 : 2	217 10	217 9
% Query Match L	100.0	69.7	59.0	57.8	87.8	57.8	57.8	57.8	57.8	57.8	57.8	57.1	57.1	57.0	56.2
Score	797	555.5	470	463	461	461	461	461	46.	461	461	455	455	454	448
Result No.	-	7	8	4	ហ	Q	7	8	6	10	c 1	12	13	14	15

Sequence 12, Appl Sequence 3, Appl Sequence 3, Appl Sequence 2, Appl Sequence 2, Appl Sequence 19, Appl Sequence 19, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 5, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 12, Appl Sequence 11, Appl Sequence 12, Appl Sequence 11, Appl Sequenc	5,
US-10-924-200-12 US-10-306-822-1 US-10-306-822-1 US-10-1043-487-3 US-10-1043-487-35 US-10-103-313-411 US-10-103-313-411 US-10-103-313-411 US-10-103-313-411 US-10-103-313-411 US-09-861-687-19 US-09-736-111-6 US-09-736-111-6 US-09-736-111-6 US-09-736-111-5 US-09-740-359-7 US-09-894-711-12 US-09-894-711-12 US-09-740-359-12 US-09-740-359-12 US-09-740-359-12 US-09-740-359-12 US-09-740-359-12 US-09-740-359-12 US-09-740-359-12 US-09-740-359-10 US-09-740-359-10 US-09-740-359-10 US-09-740-359-10 US-09-740-359-10	US-09-947-563-5 US-09-205-658-125
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	8.5 8.5 8.5

ALIGNMENTS

COMPUTER RENDABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: HM PC COMPALIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcentin Release #1.0. Version #1.30
CUSREM APPLICATION NUMBER: US/10/054.873 NUMBER OF SECUENCES: 7
CORRESPONDENCE ADDRESS:
CORRESPONDENCE TOWNSEND and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor NAME: Mycroft, Frank J REGISTRATION NUMBER: 46,946 REFERENCE/DOCKET NUMBER: 020167-000136US PRICK APPLICATION DATA:
APPLICATION NUMBER: WC PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
ATTORNEY/AGENT INFORMATION: FILING DATE: 22-Jan-2002 CLASSIFICATION: <Unknown> INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACIERISTICS: LENGTH: 150 amino acids TYPE: amino acid Sequence 7, Application US/10054873 Publication No. US26020164712A1 San Prancisco STATE: California CCUNTRY: USA 21P: 94111-5834 US-10-054-873-7

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61 IPSNREETQQKSNLELLRISLLLIQSWLEPVOLGTGPRFVNQHLCGSHLVEALYLVCGER 120
                                                                1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAY1PKEQKYSFLQNP------ 49
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence
                                                                                                                                     121 GFFYTPKTRGIVEQCCTSICSLYQLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Innear NOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-16-054-873-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09984010 Publication No. US20030104578A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                              Sequence 2, Application US/10054873
Publication No. US20020164712A1
GENERAL INFORMATION: Abong Ru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 92 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 92; Conserv
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CS-09-984-010-23
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                                                                                                                                                                                                                                                                                     1 MEPTIPLSRLPDNAMLRABRLHQLAFDTYOGPFEAYTPKHOXYSFLONPOTSLSTSRSTP 60
                                                                                                                                                                                                            1 MEPTIPLSRIFDNAMIRARRIHQLAFDTYQBFBRAYIPKEÇKYSFIÇNPƏTSLSFSESIP 69
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Publication No. US20240164712A3
GENERAL INFORMATION:
APPLICARATION: Abong Ru
fills OF INVENTION: Chimeric Protein Containing an
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                                                                                                             Score 797; UR 14; Length 150;
Pred. No. 1.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATURS SYSTEM: PC-DCS/MS-DCS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NOWFER: US/10/654.973

Filing DATE: 22-Jan-2032

CLASSIFICATION: VUNROWN?
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: WC PCT/CN88/00652
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 69/423,160
FILING DATE: 11-DEC-2066
                                                                                                                                                                                                                                                                                                                                                               12% GEFYTPKTKGIVEGOCTSIOSLYGGENYCN (50
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                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ IF NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACIERISTICS:
LENGTH: 107 amino acids
STRANDEDNESS: <Unknown>
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                                                                                                               100.0%;
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STAIE: California
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                                                                                                                                                     Conservative
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                                                                                                                               Best Local Similarity
Matches 150: Conserv
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Matches 107; Conserv
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                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC Compatible
CERRATING SYSTEM: PC-DOS/KS-DGS
SOFTWARE: Patentin Rolease #1.0, Version #1.30
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 020167-000130US
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Pred. No. 1.5e-44;
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WC PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
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100.0%; Pred. No. 1.
10.0%; Mismatches
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APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIPICATION: <UNKNOWN>
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Opery Match
Best Local Similarity
Matches 102; Conserv
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                    ADDRESSEE: FINNEGEN, HENDERSON, FRANKOW, GARREIT & DOINNER, DEP
STREET: 1300 I Street, NW
APPLICANT: Ballance, Devid James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GEOMPH HOPENS
AND SEROM ALBUMAIN
                                                                                                                                                                                                                                                                                                  COMPUTER: THM PC: Compatible
COMPUTER: THM PC: Compatible
OPERATING SYSTEM: PC-DGS/MS-LGS
SOFTWARE: Patentir Release #1.6, Version #1.36 (EPG)
SOFTWARE: Patentir Release #1.6, Version #1.36 (EPG)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,016
PRIOR APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-GN-1996
APPLICATION NUMBER: PCT/GB96/03164
FILING DATE: 19-DGC-1996
INFORMATION FOR SEQ ID NO: 23:
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Publication No. US20630153003A1
GERRAL. TWORMATION:
APPLICANT: USERS A. Wells
APPLICANT: Brian C. Cunninghar.
ITILE OF INVENTION: GROW'H HORNONE VARIANTS
FILE REFERENCE: 669.12-US-7
CURRENT FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/190,864
PRIOR APPLICATION NUMBER: 08/190,864
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/190,723
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR PILING DATE: 1992-04-02
PRIOR PILING DATE: 1992-04-27
PRIOR PILING DATE: 1992-04-27
PRIOR PILING DATE: 1992-04-27
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                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopry disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: < Joknown>
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Best Local Similarity 70.3%;
Matches 102; Conservative
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                                                                         NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                               CITY: Washington
STATE: DO
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62 PSNREETOOKSNLHILRISHILLIGSWILEPVOLGTGERFVNQHLCGS------HLVE 111
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APPLICANT: Solder Biotechnology, Inc.
ITILE CM INVENTION. Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-FUS
CURRENT APPLICATION WORBER: US/US/462,941
PRIDE FILING DATE: 2003-2626
PRIDE FILING DATE: US/09/462,941
PRIDE FILING DATE: 1997 07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 191;
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PRICE FIGUNG DATE: 1989-15-26
PRICE APPLICATION NUMBER: 07/264,611
PRICE FILING DATE: 1986-10-28
SUMMER OF SEQ IL NOS: 20
SUMMER OF SEQ IL NOS: 20
SUMTWARE: FASTSEQ ICE Windows Version 4.0
SEQ ID NO 1
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Sequence 1, Application US/10400708
Publication No. US20030166865A:
GENERAL INFORMATION:
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Sequence 1, Application US/10400377
Publication No. US20030162949A1
GENERAL INFORMATION:
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SEQ ID NO 1
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: TYPE: PRT
: CRGANISM: Homo Sapiens
::S-10-153-207-1
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Publication No. 052036171284Ai
GENERAL INCENTARIEN
APPLICANT: COX 111, George N
APPLICANT: Golder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormons and Related Proteins
FILE REFERENCE: 4152-1-P05
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 05/09/462,941
PRIOR FILING DATE: 2003-61-4
PRIOR FILING DATE: 1057-07-14
PRIOR FILING DATE: 1057-07-14
SOFTWARE: PALENTION NUMBER: 60/052,516
PRIOR FILING DATE: 1057-07-14
SOFTWARE: PALENTION VOIS: 41
SOFTWARE: PALENTIN VOIS: 41
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76.3%; Pred. No. 3.4e-43;
tive 7: Mismatches 20; indels 16: Laps
                            APPLICANT: Holder Hickorhoology, Inc.
APPLICANT: Holder Hickorhoology, Inc.
TITLE OF INVENTION: Derivatives of Growth, Hormone and Related Proveins
FILE REPERENCE: 4152-1-903
CURRENT APPLICATION NUMBER: 05/10/400.708
CURRENT FILING DATE: 2003-33-26
PRIOR APPLICATION NUMBER: 65/09/462,941
PRIOR APPLICATION NUMBER: 66/052,516
PRIOR APPLICATION NUMBER: 66/052,516
PRIOR APPLICATION NUMBER: 66/052,516
NUMBER CF SEC ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 70.3%; Pred. No. 3.9e-43;
Matches 102; Conservative 7; Mismatches 20; Indels 19
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APPLICANT: COX III, George N
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Matches 102, Conservative
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US-10-400-708-1
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US-10-298-148-1
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Best Local S
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62 PSNREETQQXSNLELLRISLLLIQSWLEPVQLGTGPRFVNQALCGS-----HLVE 111
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APPLICANT: Chernykh, Svitiana I.
APPLICANT: Chernykh, Svitiana I.
APPLICANT: Slavchenko. Iryna Yu.
APPLICANT: Vozianov, Cleksandr
TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
FILE REFERENCE: PHAGE-D06A
CURRENT APPLICATION NUMBER: CS/09/929.918
CURRENT FILING DATE: 2001-08-15
PRICK APPLICATION NUMBER: 09/318,288
PRICK APPLICATION NUMBER: 09/318,288
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APPLICATION CONDIGHAM
ITLE OF INVENTYON CROWITH HORMONE VARIANTS
FILE REFERENCE: 669.12-CS-C7
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 06/479,884
FRIOR FILING DATE: 1999-00-C2
PRIOR APPLICATION NUMBER: 06/19,723
PRIOR APPLICATION NUMBER: 06/19,0-723
PRIOR APPLICATION NUMBER: 07/966,227
PRIOR APPLICATION NUMBER: 07/86,227
PRIOR APPLICATION NUMBER: 07/86,04
PRIOR APPLICATION NUMBER: 07/875,204
PRIOR APPLICATION NUMBER: 07/85,004
PRIOR APPLICATION NUMBER: 07/426,611
PRIOR APPLICATION NUMBER: 07/264,611
PRIOR APPLICATION NUMBER: 07/264,611
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SCFTWARE: FastSEO for Windows Version 4.0
SEQ ID NO 9
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Sequence 6. Application US/10153267
Pub.:Cat.Cm. No. US20630153603A1
GENERAL: NFORMATION
APPLICANT: James A. Wells
APPLICANT: Brian C. Cunningham
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Nest Local Similarity 70.38
Matches 102, Conservative
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OS 10-153-207-6
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US-09-929-918-9
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Sequence 4, Application 05/0969748C Publication No. US20030161809A1 GENERAL INFORMATION:
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Best Local Similarity 69.79
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                      : TYPE: PRT
: ORGANISM: Homo sapiens
US: 09-853-686-2
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                                                                                                                                                                                                                                                     LENGTH: 217
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Sequence 66. Application US/09280230A
Sequence 66. Application US/09280230A
Sequence 66. Application Sequence 67.
General information.
APPLICANT: Siquential Nachiko
APPLICANT: Fiquential Nachiko
APPLICANT: Fiquential Nachiko
APPLICANT: Foldo, Toshiyuki
APPLICANT: Mudo, Toshiyuki
APPLICANT: Kondo, Masaka
IIILE OF INVENTION: PREPARING USEFUL PULYPEPLIDES THROUGH EXPRESSION OF THE PREPARENCE: 382.1026
CURRENT APPLICATION NUMBER: US/09/280,030A
SMRENT APPLICATION NUMBER: US/09/280,030A
SMRENT APPLICATION NUMBER: JP10.87339/1998
SARLIER PILING DATE: 1999-03-36
SARLIER FILING DATE: 1999-03-36
SARLIER FILING DATE: 1999-03-31
SOFTWARD FILING DATE: 1999-03-31
SOFTWARD FILING DATE: 1999-03-31
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HTH GITH CHILL CHILL THICK
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                                                                                                                                                         2. PPTIPISKLEDNAMIKAHRIEQIAAFOTVQEFERAYTEKEQKYSFIQNEGTSLGESESTET ()
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APPLICANT: PROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
ITILE OF INVENTION: METHOD FOR DETECTING GROWTH HORNGNE VARIATIONS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Description of Artificial Sequence: Lesignaturé 18 O'OFFER INFORMATION: an amino acid sequence of MWFSp-WWFHP26-7EV-G-SHUS-09-280-030-66
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    57.8%; Shore 461; OB htt Tendon 217;
70.8%; Pred. No. 4.6h-43;
                                                                                       Stelen:
                                                                                   7; Mismatches
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Patent No. US20320081605Ai
GENERAL INFORMATION:
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SEO ID NO 66
LENGTH: 245
Query Match
Best Local Similarity 70.33
Matches 102; Conservative
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Best Local Similarity 70.37
Matches 102; Conservative
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APPLICANT ARIZEKS PHARMACETTICALS, INC.
APPLICANT HUGSTON, Lou, L.
APPLICANT HUGSTON, Lou, L.
APPLICANT HUGSTON, Lou, L.
APPLICANT SHERIDAN, Philip, J.
APPLICANT HAWEN, Stephen
APPLICANT GIYNN, Zacqueline, M.
APPLICANTON: AGENTS ACROSS CELULAR BARRIERS
FILE REFERENCE: 057220-0303
CURRENT FILING DATE: 2001-02-09
FRIOR PILING DATE: 2001-02-09
FRIOR PILING DATE: 2000-11-13
FRIOR FILING DATE: 2000-11-13
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69.7%; Pred. No. 2.1e-42;
Live 7; Mismatches 21; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.1%; Score 455; DB 9; Length 217; Best Local Similarity 69.7%; Pred. No. 2.1e-42; Matches 101; Conservative 7; Mismatches 21; Indels
TITLE OF INVENTION: HOMANS, THE VARIATIONS AND THEIR USES FILE PRESENCE: WOM78
CUCHENT APPLICATION KIMBER: 38/39/853,688
CUCHENT APPLICATION FORE: 2001-05-14
NUMBER OF SED ID NOS: 66
SOFTWARE: PATCHLIN Ver. 2.1
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3(HHL) HITTHILLIH HITTHILLIH 1111 1111 11 11 11 11 12 PPITPLSRPFDNAMIRARRHOLAFOTYQEPRAATFKKOKYSELQNPQISKRESESIFI 66
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Patent No. US20020681605A1
GENERAL INFORMATION:
APPLICANT: COOPER, DAVID N.
APPLICANT: GREGORY JOHN
APPLICANT: MILLAR, DAVID S.
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HERMONE VARIATIONS IN TITLE OF INVENTION: METHOD FOR USAND TITLE OF ENVENTION: METHOD FOR USAND TITLE OF ENVENTION: METHOD FOR USAND TITLE OF STORMAN APPLICANT: NUMBER: US/39/853,638
CURRENT APPLICANTON NUMBER: US/39/853,638
CURRENT APPLICANTON NUMBER: US/39/853,638
COURRENT PALENCY OFFE: 2001-05-14
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                    Sequence 16, Application US/39E04439A
Patent No. (022032)55100A1
GENERAL INFORMATION
APPLICANT: KIEFER, TIMOTHY J.
APPLICANT: CHEUNG, ANTHONY T.
TITLE OF INVENTION: COMPOSITIONS AND METHOES FOR RESULATED PROTEIN
ITLE OF INVENTION: CAPESSION IN GIT
FILE REFERENCE: 029996/C27 8721
CURRENT APPLICATION NUMBER: US/39/804,409A
CURRENT FILING DAIE: 2001-03-12
NUMBER OF SEC IN 00S: 18
SOFTWARE: PATENTIN VEI. 2.1
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69.7%; Pred. No. 2.86-42;
tive 7; Nismatches 21; Indels 17
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              112 ALYBVCG -- ERGFFYTPKIRGIVEQ 134
                                          146 GIQTLMGRLEDG---SPRIGOTFKQ 167
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Best Local Similarity 69.77
Matches 101; Conservative
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US-09-853-688-4
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LENGTH: 217
TYPE: PRT
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TYPE: PRI
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September 16, 2003, 12:36:15 : Search time 17.5097 Servads (Willion: alloaments) 825:845 Million cell updates/ser Run on:

US-09-423-100-7 797 1 MPPIRPLSRLEDNAMLRAHR.....IVEQCCTSICSINGLENYON 150

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapoxt 0.5 Scoring table:

283308 segs, 95158682 residues Searched:

283308 Total number of hits satisfying thosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 130% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	J.	STHC	167410	STHUV	STHUV2	167409	:6741.	157408	153267	LCHUC	E32435	A26449	B49159	PN0140	STHO	STMS	STRT	849483	JK0219	STPG	I46:45	JC4632	A37782	A61584	JS0429	STRO	STSH	STGI	S32682	JC1514
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	Length	217	217	217	256	217	2:7	212	217	217	2:3	215	21.6	067	351	216	216	216	190	216	216	216	216	190	190	217	217	217	217	216
ص	249	57.8	57.73	53.5	53.5			49.7	49.7		47.8	45.1	39.0	38.6	œ,	·Y.	:12	38.0	~	r-	7	7	r-	7	r>	35.3	36.3			34.9
	Score	191	460	426.5	426.5	407.5	405	396	398	381	38.	359.5	310.5	307.5	306.5	304.5	302.5	302.5	301.5	- 1	301.5	301.5	299.5	297.5	295.5	289.5	289.5	289.5	289.5	278.5
	Result No.	-	2	3	.,	ហ	•	7	œ	ō	10	11	12	13		15	3.6	17	18	19	20	21	22	23	24	25	56	27	28	29

insulia precursor	insulic precursor	somatotropin precu	epidermal growth t	insulin - sperm wh	insulin - fimback	insulin - elephant	insulia precursor	insulin precursor	insulin - hamster	insulin precursor	insulin - Eqyptian	somatotropin - dre	insulin precursor	insulin precursor	insulin precursor
: NRB	B42179	A50509	PC7082	IMMHP	TWWHF	INEL	JQ6278	A42179	INHY	IPHU	INMSSP	A60625	A59151	1980	148166
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34.8	34.8	34.6	34.5	34.3	34.3	e . 48	34.3	34.1	34.1	33.8	33.7	33.7	33.6	33.4	33.3
277.5	277.5	275.5	275	273.5	273.5	273.5	273.5	272	271.5	270	268.5	268.5	267.5	266.5	265.5

ALIGNMENTS

RESULT 1 STHU	
somatotropin N;Alternate n N;Contains: g	<pre>l precursor [validated] - human ames: growth hormone 1; hGH-N; pituitary somatotropin growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1, s)</pre>
C.Date: 24-Ap C.Date: 24-Ap C.Accession: R.DeNoto, P.M	spects. Gaussius (main) Cidate: 24-Apr.1984 *sequence_revision 10-Feb-1895 *text_change 08-Dec-2000 C:Accession: A93731; A32435; A93694; A94247; A90051; A93397; A93778; A91764; A90217 *X:Devoto, P.M.; Moore, D.D.; Goodman, H.M.
Auther Actua Arither Huma Arketerener ArAccession: ArMolecule ty	nes. 9, 37.37-37.30, 1301 an growth hormone DNA sequence and mRNA structure: possible alternative number: A93731: MUID:82014939; PMID:6269091 A93731 Pe: DNA
A:Cross-refer A:Note: the 2 R:Check E:Y:	As Fessidics: 1-217 (DEX) As Tooss-reforences: CB: V00520 As Note: the 20K short form sommatotropin lacks residues 58-72 (32-46 in the active home the constant form sommatotropin lacks residues 58-72 (32-46 in the active home the constant form sommatotropin lacks residues 58-72 (32-46 in the active home the constant form some form the constant form the
Concerce 4. 479-497, 199 A.Title: The human grown A.Acterence number: A324 A.Accession: A32435 A.Molecule type: DNA	. 19-497, 1959 human growth hormone locus: nucleotide sequence, biology, and evolution sumber: A32435; MUID:89307277; PMID:2744760 A32435 pe: DNA
A;Cross refer	A)Residues: 1-217 <che> A(Cross-references: GB:J03071; NID:g183148; PIDN:AAA52549.1; PID:g183149</che>
Rigoskan, W.; Rouge Nucloid Anids Res. Aritle: Molecular A;Ruference number: A,Ancession: A93694	KiRoskan, W.; Rougeon, F. Nucloic Anids Res. 7, 365-320, 1979 Nucloic Anids Res. 7, 365-320, 1979 AlPelerone number: A53594; MUID:80034477; PMID:385281 A.Ancession: A93694
A:Molecule type: mRNA A:Residues: 1-217 <rgs> A:Cross-references: GB: A:Mote 35-pro was also R:Martal, d.A.: Hallew</rgs>	A:Molecule type: mRNA A:Russides: 1-217 <rgs> A:Cross-references: GB:V00519 A:Rote: 35-For was also found R:Martial, J.A.: Hallewell, R.A.: haxter, J.D.: Goodman, H.M.</rgs>
Science 205, 602-607 A:Tille: Human growth A:Reference number: A:Accession: A94247	Science 265, 602-607, 1979 Actionce 265, 602-607, 1979 Actionce Ethman growth formone: complementary DNA cloning and expression in bacteria Action Number: A94247, MUID:79203293; PMID:377496 Accession: A94247
A Molecule type: mRNA Alsesidues: 1-217 AMAR KLL. C.H., Dixon, J.S Krch. Biochem. Biophys A Title: Bixman pituita A Reference number: Age A.Contents: annotation	A:Wolecule type: mRNA A)Rashducs: 1-217 cMRNA A)Rashducs: 1-217 cMRNA Arch. Biochem. Biophys. 133, 76-91, 1969 Arch. Biochem. Biophys. 133, 76-91, 1969 ArTitle: Burman pituitary growth hormone. XIX. The primary structure of the hormone. A:Contents: annotation
Kili, C.H.; Dixon, J.S. Arch. Blocken. Bixon, J.S. A.Tillo: Human pitulidary A.Reference number: A900 A.Accession: A90051 A.Molecule type: protein	%:li., C.S.: Dixon, J.S. Arch. Blochys. 146, 233-236, 1971 A:Title: Human pituitary growth hormone. XXXII. The primary structure of the hormone A:Reference number: A90051; MUID:72143935; PMID:5144027 A:Recession: A90051
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Nialtornate names: growth hormone (Species: Macadam acadam) Species: Macadam culatta (ricsus macadam) (Species: Macadam culatta (ricsus macadam) (Species: Macadam) (1999 - 13-May-13-May-13-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13-May-13
C:Comment: The gene for this hormone is transcribed only in somatotrophic cells C:Comment: About 90\% of somatotropin is the 22K long form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85
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                                                                                                                                                                                                                                                           A Map position: 17q23.1-17q23.3

A Introns: 4/1; 57/3; 97/3; 152/3

A Suberidamily: prolaction

C: Superidamily: prolaction

C: Keywords: alternative splicing, hormone: pituitary

F: 26/20main: signal sequence *status predicted <SIG>

F: 27-21/Product: somatotropin 1, long form *status experimental <SOL>

F: 27-57,73-217/Product: somatotropin 1, short form *status experimental <SOS>

F: 27-57,73-217/Product: somatotropin 1, short form *status experimental <SOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FPTIPLSKLFDNAMLRAHRLHQLAFUTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 FPIIPLSRLEDNAMLKAHRLHGLAFDTYQEFEFAYIPKEQKYSFLQNPQTSLCFSESTPT
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A:Molecule type: mkNA
A:Molecule type: mkNA
A:Residues: 1-217 <RES.3
A:Cross-references: GB:L16556; NID:q293114; PIDN:AAA18842.1; PID:q293115
A:Cross-references: GB:L16556; NID:q293114; PIDN:AAA18842.1; PID:q293115
B:L1, C.H.; Chung, D.; Lahm, H.N.; Stali, S.
Arch. Biochem. Biophys. 245, 287-291, 1986
A:Title: The primary structure of monkey pituitary growth hormone.
A:Reference number: A05094; MUID:86129460; PMID:3080959
A:Accession: A05694
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Accordents: amnotation: identification of source organism cisuporfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 461; DB 1;
Pred, No. 7.5e-38;
7; Mismatches 20:
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A:Residues: 27-99, 0',10:-178, D',180-217 <LIC>
A:Note: the monkey species is not identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSNREETQOKSNLELLKISLLLIQSWLEPVQ 92
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A.Cross-references: GDB:119982; OMIM:139250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 ALYLVCG--ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%; 70.3%;
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A Molecule type: protein
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A Residues: 27-34, 12, 36-47 <8085
R. de Vos, A.M.: Ultsch, M.: Kosslakoff, A.A.
R. de Vos, A.M.: Ultsch, M.: Kosslakoff, A.A.
Science 255, 306-312, 1992
A.Title: Human growth hormone and extracellular domain of its roceptor: crystal structure counber: A4-728; MULD-92196577; PMIDH-1549776
A.Reference number: A4-728; MULD-92196577; PMIDH-1549776
A.Reference counber: A7-728; MULD-92196577; PMIDH-1549776
A.Roceston: Lis Baldridge, J.S.; NCKeown, K.S.: Heyneker, H.L.; Chang, C.N.
Gene 39, 247-254, 1985
A.Title: Periplasmic production of correctly processed human growth hormone in Escherich A.Reference number: 14-126; MULD-18613793; PMIDH-8912691
                                                                                            Nature New Biol. 230, 90-91, 1971
Astricte: Revised primary structure for human growth hormone.
Astrictes anumbor: A93397 MUID:71139765; PRID:5279946
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A:Molecule type: mRNA
A:Residues: 1-26 <RES>
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A; Molecule type: protein
A; Residues: 119:120;157:159 < N12>
A;Residues: 27.94;96-217 <LIC>R;Niall, H.D.
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chorionic sumatonammotropin-3 - rhesus macaque
Cispecies: Macaca mulatia (rhesus macaque)
Cibato: Macacas mulatia (rhesus macaque)
Cibato: 13-May-1996 Fsequence_revision 31-May-1996 #text_change 16-Jui-1999
Cibato: 16-May-1996 Fsequence_revision 31-May-1996 #text_change 16-Jui-1999
Cibatocas in 16-409
Riccios, 7.6.: Durning, M.: Fisher, J.M.; Fowler, P.D.
Endocrinciogy 133, 1744-1752, 1997
Alittle: Cloning of four growth hormone/chorionic somatomammotropin-related complement is 153267; MJID:94008724; PMID:8406617
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Parcossion: A280725; Murd: 88243769; PMID: 3379057
PArcossion: A28072
PMID: A28072
PMID
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                                                                         A:Status: preliminary, translated from GB/EMBL/DDBJ
A:Molecule type: mkNA
A:Residus: 1-217 <REA
A:Crossreferences: GB:L16554; NID:g293112; PIDN:AAA18841.1; PID:g293113
O:Superfamily: prolactio
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            ---GTGPRFVNOHL 104
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F:1-26/Domain: signal sequence *status predicted <SIG>
F:27-256/Product: somatotropin 2 splice form 2 *status predicted <MAI>
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            62 PSNREETQQKSNLEL.RISLLLIQSWLEPVQL----
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A/Cross-references: GDB:119963; OMIM:139240
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A:Eutrons: 4/1: 57/3: 97/3: 152/3
C:Superfamily: prolactin
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Matches 89;
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Ny Indonestic names: growth hormone 2; growth hormone varions 2; such spiles (how sapisons (man)).

C) Date: 17-Dec 1962 (sequence revision 10-Feb 1963 (next_charace 2) Any 10-63 (charcession).

C) Accession: D32435; B28072; A31511; IS2164; A6071;

R) Cher. E. Y. Tido, Y. C., Smith, D.B.; Barrera Saldana, B.A.; Gelinas, B.E.; Sectora 9. R. Genomics, 4. 479-497, 1963 (man) and exclusion of a sectoral number: A3245; MUID:83307277; PMID:2744763 (man) exclusion.

A) Reference number: A3245; MUID:83307277; PMID:2744763 (man) exclusion.

A) Residues: 1.217 COHE>
A) Cobs. references: GB:J03071; NID:9183148; PIDN:AAA52552.1; PHD:9183152 (man) planenta A; Reference number: A92725; MUID:88243769; PMID:377967 (man) in the furner planenta A; Reference number: A92725; MUID:88243769; PMID:377967 (man) E28072 (man) A; Residues: 1.217 COC>
A; Residues: 1.217 COC>
B; Seeburg, P.H.
By Seeburg, P.H.
By Seeburg, P.H.
By Seeburg, P.H.
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A.Reference number: ACISII MUDD: $3182010; PMID:7155309

A.Reference number: ACISII MUDD: $3182010; PMID:7155309

A.Residues: 134 'P' 56-217 <SEE>

A.Reterence number: 152104

A.Reterence number: 15
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PSNRBETÇQKSNLELLRISLLLTQSWLEPVQ 117
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A:Reference number: 153267; MUID:94008724; PMID:8404617
A:Accession: 153267
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A:Rosidios: 1-217 COURS
A:Cross-retorences: GB:C03071; NID:g183148; PIDN:ANA52551.1; PID:g183151
R:Goodman; H:M.; DeNoto, F:; Fiddes: J.C.; Hallewell, R:A:; Page, G.S.; Smith, S.; T
In Mobilization and Reassembly of Genetic Information, Scott, W.A.; Werner, R., Jose
A:Reference number: A94422
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A. Molecile type: MRNA
A. Residues: 1-3 <TANN
A. Cross-references: GB: M35419; NID: 9506822
A. Cross-references: GB: M35419; NID: 9506822
A. Sherwood, L.M.; Burstein, Y.: Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 76, 3819-3823, 1979
A. Title: Primary structure of the NH-2-terminal extra piece of the precursor to hum?
A. Reference number: A93833; MUID: 80034970; PMID: 291043
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A:Residues: 1-217 <600>
B:Tanaka, M.: Masuda, N.: Watahiki, M.; Yamakawa, M.: Shimizu, K.; Nagai, J.; Nakash
B:Ochem. Int. 15, 287-292, 1988
A:Title: cDNA cloning of human chorionic somatomammotropin-I mRNA whose transcriptic
A:Reference number: I52342; MUID:88269096; PMID:2835050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A:Molecule type: mRNA
A:Rusiluss: 1-217 <RES-
A:Crossreferences: GB:L16552; NID:g293108; PIDN:AAA18839.1; P1D:g293109
C:S:perfamily: prolactin
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A:Residues: 1.3-26 <SHE>
A:Experimental Source: placenta
A:Experimental P.H.; Martial, J.A.; Baxter, J.D.; Goodman, H.M.
R:Shine, J.; Seeburg, P.H.; Martial, J.A.; Baxter, J.D.; Goodman, H.M.
Nature 270, 494-499, 1977
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R:Li, C:E.; Dixon, J.S.; Chung, D.
Arch. Biochem. Biophys. 155, 95-110, 1973
A:Title: Amino acid sequence of human chorionic somatomammotropin.
A:Feference number: A90054: MUID:73201971; PMID:4712450
A:Accession: A90054
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A:Residues: 50-217 <SHI>
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Best Local Similarity
Matches 74; Conserv
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St. C. During, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A:Title: Cloning of four growth hormone/chorionic scmutomammotropim-related complementations and the scenario number: 153267; MJID:94038724; PMID:8464617
A:Accession: 167411
A:Status: preliminary: translated from GB/EMBs./DD3J
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Endocrinology 13, 1744-1752, 1993
Arfitle: Cloning of Four growt: hormone/chorionic somatomamotropin-related complementar
A:Reference number: 153267: MUID:94068724; PMID:8404617
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CiSpecies: Macaca mulatta (rhesus macaque)
CiDacies: Jamy-1996 #sequence_revision 31-May-1999 #rext_change [6-Ju]-1999
CiAccession: 153267 | Region of the complete of the comp
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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-101-1359
C;Accession: 167408
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A;Residues: 1-12.2 <RBS:
A;Cross-references: 08:LL6553; NID:9293110: PIDN:AAA!8843:1: PID:9293:11
C;Superfamily: prolactio
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A;Rosidudes: 1-217 CRES-
A;Cross-references: GB:116555; NID:q293116; FIDN:AAA20186.1: PID:g293117
C:Superfamily: prolactio
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82.2%; Pred. No. 1.8e-31;
Live 11; Mismatches 5; Indels
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Best Local Similarity 67.7%; Prod. No. 2.4e-32;
Matches 86; Conservative 9; Mismatches 18;
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                                                                                                                                                                                                                                                            N;Alternate names: growth hormone
C;Species: Macaca mulatta (rhesus macaque)
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Matches 74; Conservative
                                                                                                                                                                                                             somatotropin - rhesus macaque
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Query Match

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Cisportes: Horo sapiens (man)
Cisportes: Horo sapiens (man)
Cisportes: 29-Dec-1889 *sequence_revision 29-Dec-1989 *text_change 16-Jul-1999
Cisportes: 29-Dec-1883 *sequence_revision 29-Dec-1989 *text_change 16-Jul-1999
Sichen, E.Y. Jaco, Y.C., Smith, D.H., Harrera-Saldana, H.A.: Gelinas, R.E.: Seebur Genomics 4, 479-497, 1989
A.Title: The human growth hormone locus: nucleotide sequence, biology, and evolutio A.Reference number: A32435 MUID:89307277; PMID:2744760
A.Accession: E32435
A.Status: preliminary
A.Molecule type: DAS
A.Status: Preliminary
A.Molecule type: DAS
A.Status: CHEPA
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C.Species: Juni 1988 *sequence_revision 30-Jun-1988 *text_change 28-Jul-1995
C.Bacession: A56449
F.Hitt, H.: Kimelman, J.; Birnbaum, M.J.; Chen, E.Y.; Seeburg, P.H.; Eberhardt, N.L.
INNA 5, 54-70, 1987
A.Stille: The human growth hormone gene jocus: structure, evolution, and allelic var
A.Reference number: A26449; MUID:87161235; PMID:3030680
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0:Superfamily: prolactin
E:1-26/Nomain: signal sequence *status predicted <SIG>
E:27-215/Product: choriomammotropin, hGS-3 allele *status predicted <MAT>
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Pred. No. 5.4e-30;
8; Mismatches 8;
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MyAlternate names: chorionic somatomammotropin 2
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C:Superfamily: prolactin
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A:Molecule type: DNA
A:Residues: 1-215 <HIR>
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A; Mesidias: 27-277 cMTA
A; Residias: 27-277 cMTA
A; Residias: 27-277 cMTA
A; Residias: 27-277 cMTA
Biochem. Soc. Trans. 19, 278, 1991
A; Mille: Catechol-C-mothyltransferase from human placenta: purification and some propert
A; Reference number: A91283; MUID:91244C06; PMID:2037146
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Asture New Biol. 233, 59-61, 1911
A;Title: Amino-acid sequence of 'uman placental lactocen.
A;Reference number: A93401; MUID:72016313; PMID:5286363
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R.Sherwood, D.M.; Handworger, S.; McLaurin, W.D.; Lanner, M.

Nature New Biol. 235, 64, 1972

A.Reference number: 949465

A.Contents: amootation

R.Schnedder, A.B.; Kowalski, K.; Russell, J.; Sherwood, D.M.

A.Contents: amootation of the interchain disulfide bonds of dimeric human placental la A.Reference number: A2225; MUTD:9473681; PMID:438159

A.Title: Identification of the interchain disulfide bonds of dimeric human placental la A.Reference number: A2251; MUTD:9713681; PMID:438159

A.Contents: amootation; dimeric disulfide bonds

R.Seiby, M.J. Barta, A.: Baxter, J.D.; Beil, G.I.: Eberhardt, N.D.

J. Biol. Chem. 259: 1332-1338, 1984

A.Title: Analysis of a major human chorionic somatomampetropin gene. Evidence for two: A.Reference number: 155229, MUD:85030426; PMID:6238192
                                                                                                                                                                                     in Prolactin and Carcinocenesis, Proc. Fourth Tenemus Workshop Prolactin, Griffits. A.Title: The chemistry of the human lactocenie bermanes. A.Reference number: A94427 A.Reference number: A94427
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Eji-26/Domain: signal sequence Estatus experimental «SIG»
Eji-26/Domain: choriomammotropin A Fstatus experimentai "MAT»
Eji-21/Posulfide bonds: Estatus experimental Eji-208-215/Disulfide bonds: In monomeric form) #status experimental
Fj208-215/Disulfide bonds: Interchain (to 215 in directe form) #status experimental
Fj208/Disulfide bonds: Interchain (to 208 in dimeric form) #status experimental
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A Status: translated from GB/EMBL/DDBJ
A Molecule Lipor-TRNA
B Residues: Lipor-TRNA
B Residues:
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47.8%; Pred, No. 5.44+30;
3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 17922-17924
A;Introns: 4/1; 57/3; 97/3; 152/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 82.0%;
Matches 73; Conservative
                                                                                                          A, Experimental source: placenta R; Niall, H.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 27-46 <NIC>
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A; Residues: 1-217 <RES>
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somatotropin - golden hamster

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Rizakin, M.M.: Poskus, E.; Deliacha, J.M.; Paladini, A.C.; Santome, J.A.
FEBS Lett. 25, 77-82, 1972
A:Title: Amino acid sequences around the cystine residues in equine growth hormone.
A:Reference number: A31383
                                                                                                                                                                                                                                                                                                                                                                                                  Alacession A91383
Alacession A91383
Alacession by the protein
Alacessides 42-69,157-190 <2A3>
Blocker, 5.1 Sartree, A.S.
Blocker, J. 199, 19-24, 1968
Alfille, Amino acid sequences around the cystine residues in horse growth hormone.
Alfecterance number: A90240; KUID:68368390; PMID:4876100
Alacession: A90240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FPT:PLSRLFDNAMLRAHRLHQLAFDIYQEFBHAYIPKHOKYSFLQNPQTSLSFSHSIPT
   A:Moleculc type: protein
A:Residucs: 1-190 <ZAK>
A:Residucs: 1-190 <ZAK>
A:Zakīn, M.M.; Poskus, E.; Dellacha, J.M.; Paladini, A.C.; Santome, J.A.
FEBS Lett. 34, 353-355, 1973
A:Tet.c: The amino acid sequence of equine growth hormone.
A:Reference number: A91395; MUID:74020362; PMID:4747849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Molecule type: protein
A:Residues: 176-190 (OLI>
0:Moperfamily: prolactin
0:Reywords: hormone: pitaltary
F:52-163,180-188/Disulfide bonds: *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 38.5%; Score 366.5; DB 1
Hest Local Similarity 65.2%; Pred. No. 9.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PSNREETQQKSNLEDLRISDLDQSWLEPVQL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  somatotropin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 64.89
Matches 59; Conservative
                                                                                                                                                                                                                      A:Molecule type: protein A:Residues: 1-190 <ZA2>
                                                                                                                                                                                     A:Accession: A91395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matiches
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                      C;Species: Mesocricetus auratus (golden hamster)
C;Date: 19-Dec-1993 resquence_revision 18-Nov-1994 rtcxt_change 21-Jui-2000
C;Accession: B49159
R;Southard, J.N.; Sanchez-Jimenez, F.; Campboll, G.T.; Talamantus, F.
Endocrinology 129, 2955-2971, 1991
B,Title: Sequence and expression of hamster projactin and arcwth hormone messenger RNAs. A;Reference number: A49159; MUID:32063850; PMID:1954881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ.
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Cibate: 13-01:1981 *Requence_revision if Jul-1981 *text_change [3-Aug-1996]
Cibates: 13-01:1981 *Requence_revision if Jul-1981 *text_change [3-Aug-1996]
Cibatession: A9:772: A9:1395: A9:3495: A0:405: A0:1581
R:Zakin, M.M.: Poskus, E.: Langton, A.A.: Ferrara, F.: Santome, J.A.: Definion, J.A.: Definions, J.A.: Definions, J.A.: Trueller Protein Res. 6: 455-444, 1376
A:Title: Primary structure of equine growth hormone.
A:Reference number: A9:772: MUID:7005419: PMID:96:15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 FPAMPLSSLEANAVLRAQHLHQIAADTYKEFERAYIPEGURYS-IQNAUTAFOFSETIPA FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FPAMPLSSLFANAVLRAQHIHELAADIYKSFERAXIFSSCRY-FLQNAQSTGCFSEVIPT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPT1PLSRLFDNAMLRAHRLHQLAFDTYORFFEAY1PKEQKYSFLQNEGTSLSFSESTET AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NyAlternate names: growth horegone
C;Species: Balachoptera borealis (sel whale)
C;Date: 07-May-1993 #sequenco_revision 07-Kay-1993 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FPTIPLSRIEDNAMIRABREHQLAFDTYQEPBBAYIPKBOKYSFLONPQTSISFSBS;PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SC 25
                                                                                                                                                                                                                                                                       A)Status: preliminary
A,Molecule type: mRNA
A;Residues: 1-216 <SCGA-A;Residues: 1-216 <SCGA-A;Cross-references: GB:S66299; NID:g239355: PIDN:AAB20368.1; PID:g239355-A;Note: Sequence extracted from NCBI backbone (NCBIN:66299; NCBIP:66300)
C;Supertamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.0%; Score (10.5; DB 2; Length 216:
67.0%; Pred. No. 4.60-23;
artive 13; Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Accession: PN0140
R:Yudaev, N.A.; Pankov, Y.A.; Bulatov, A.A.; Gsipova, J.A.
Bichtimita 47, 2059-1069, 1982
A;Title: Amino acid sequence of sciwhale somatotropin.
A;Reference number: PN0140; MUID:83000659; PMID:7115913
A;Accession: PN0140
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67.0%; Pred. No. 7.7e-23;
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A)Residues: 1-190 <PUD:
A)Note: article io Russian with English abstract
C)Superfamily: prolation
C)Superfamily: prolation
C)Keywords: growth factor; hormone
F)52-163,160-188/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PANKDEAQQRSDVELLRFSLLIQSWLGPV9 90
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N; Alternate names: growth hormone
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Best Local Similarity 67.0%
Matches 61: Conservative
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nes 61, Conservative
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61

Length 190; Indels

DB 1;

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Widiternate names: growth hormone (Species Washington) with text_change 28-May-1999 (Species) was musculus (house mouse) (Species) was musculus (house mouse) (Share: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 28-May-1999 (Share: 30-Sep-1987 #sequence) (Share: 20-1-H); Taiummantes, F. (Shares: 20-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Residues: 1-216 cills
A.Cross-references: GB:X02891, GB:X03232, NID:g51067, PIDN:CAA26650.1, PID:g51068
G.Superfamily: prolactin
G.Keywords: anterior pituitary; growth factor; hormone
F:1-26/Fommain: signal sequence #status predicted <SIG>
F:27-226/Forduct: somatotropin #status predicted <SIG>
F:78-189,206-214/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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PIGKDEAQQRSDMELLRFSLLLIQSWLGPVQL 91
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Genlore version 5.1.6
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using swincdel protein search, protein -

September 16, 2003, 12:33:30 Run on:

C.; Search time 11.67s2 Seconds (without aliqueents) 664.293 Million cell updates/sec

1 MPPIIPLSRLFDNAMLRAHR......IVEGGGTSIGSLYQLENYGN US-09-423-100-7 Title: Perfect score: Sednence:

BLOSCM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying thosen parameters:

Minimum DB seq lenath: C Maximum DB seq length: 2000366000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match O%

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escription	Pol241 homo sappen	6 pan t	٠,٠,٠	, es		_	P01242 home sapien	٠.	P01244 homo sapien		P33092 bulaenopter			C9qmh2 ayettoebus		P46407 orygetolaggs		c)	Can.S. Fa		Pli248 sus serefa	P19795 musteld cis	PR7885 lama quante	P10766 valpes valp	094160 monodelphis	0.62754 triorismis	7	P56437 cervus elab	~	~	P22077 meleadris g		P01311 oryctolagus
SUMMARIES	GI	SOMA_HUMAN	SOMA_FANTR	SOMA_MACMU	SOMA_SAIBB	SOM2_PANTR	SOMA_CALJA	SOME_HUMAN	SOM2_MACMU	PILHUMAN	SOMA_MESAU	SCMA_BALBC	SOMA_HORSE	SOMA_CALSE	SOMALNYCPY	SOMA_MOUSE	SOMA_RABIT	SOMA_RAT	SOMA, LCXAP	SOMA_CANFA	SOMA_FELCA	SOMA_FIG	SOMA_MUSVI	SOMA_LAMPA	SOMA, VULVE	SOMA_MONDO	SOMA_TRIVU	SOMA_BOVIN	SOMA_CEREL	SOMA_SHEEP	SOMA_BUBRU	SOMA_MELGA	INS_CERAE	INS_RABIT
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SOWA_HUMAN STANDAKD; PRT; 217 AA.
F0124: O4405; O16651; C9HBZ1; O9UMJ7; Q9UNL5:
21-JU5:-1886 (Fel. 0): Created)
O1-MAK-1992 (Rel. 2): Last sequence update;
15-SEP-2003 (Rel. 42) Last annotation update)
Somatciropin precursor (Growth hormone) (GH) (GH-N) (Pituliary growth hormone) (GHOKT: hormone) 1):
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MIDILINE-79603293; PubMed-37456;
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"Human growth hormone, DNA sequence and mRNA structure: possible
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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Chen E.Y., Lidao Y.C., Smith D.H., Barrera-Saldana H.A.,
Gellnas R.E., Secburg P.H.;
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Seeburg P.H.;
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SECTENCE FROM N.A. (ISOFORM 1).
MEDLINE-80034477; Pubmed=386281;
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DEAMIDATION OF GIN-163 AND ASN-178
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MEDLINE-99321812; PubMed*10393484;
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    TISSUE-Fituitary:
MEDLINF-2040257: PubMed-16431946:
Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Buang Q.-B., Ren S.-X.,
Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Buang Q.-B.,
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axis and inil-longuh convenient."
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MEDLINE-71139765; PubMed-5279046;
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MEDLINE=80130196: PubMed=7356479;
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              SEQUENCE FROM N.A. (ISCFORM 4).
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MEDLINE-95075462; PubMed-1984244;
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28-F5B-2003 (Rel. 41, Last. Sequence update)
28-F5B-2003 (Rel. 41, Last. annotation update)
Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pitultary growth
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan
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SUBCELLUCIAR LOCATION: Serreted.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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Pred. No. 4.6e-38;
Score 461) DR 1;
Pred. No. 4.66-58;
7: Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 ALYLVCG--ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PSC0266; SOMATOTROPIN_:: 1.
PROSITE: PS0C338; SOMATOTROPIN_2: 1.
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InterPro; IPR601460; Somatouropin.
Pfam: FF00103; hormone: 1.
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    57,8%;
70,3%;
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    Ouery Match
Best Local Similarity 70.3
Matches 102: Conservative
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P58756:
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SEQUENCE
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SOMA_PANTR
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2 FPTIPLSRLEDNAMLRARRIHQLAFDTYQEFBEAYIPKECKYSFLQNPQISLSFSESIPT

Sileo

16:

Indels

Mismatches

Matches 102; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-94008724; PubMed-8404617;
Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Closing of four growth hormone/chorionic somatomammotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the risesus monkey placenta.";
Endocrinology 133:1744-1752(1993).
                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Eukaryota, Metazca: Chordata, Craniata, Vertobrata, Euteleosfomi;
Mammalia; Futheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SINGCELLUIAR LOCATION: Socreted.
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BY SIMILARITY.

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E -> Q (IN REF. 2).

N -> D (IN REF. 2).

W; 2C5180341EFC46D0 CRC64;
                                                                                                                                                                                                                                        (Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                     217 AA
146 SIQILMSRLEDG---SPRTGQIFKQ 167
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#SSP: PG1241; 1AXI.

InterPro: IPRG01450; Somatotropin.
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                                                                                                                                                                                                                                                                                                                              hormone) (Growth hormone 1).
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                                                                                                                                                     STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae, Macaca.
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268
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217 AA:
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SEQUENCE OF 27-217.
                                                                                                                                                                                                                                        :-1994 (Rel.
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                                                                                                                                                                                                                                                                28-FEB-2003
                                                                                                                                                     SOMA_MACMU P33093;
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CONFLICT
SECUENCE
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                                                                                        ASSOLT 3
SOMA_MACMU
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                                                                                              2 FPT1PLSRLFDNAMLRAHRLHGLAFOTYOBFEEAYIPKEQKYSFLONPGTSLSFSESTFT #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIZER-21265436; PubMed-11271582; MEDIZER-21265436; PubMed-11271582; Liu J.C., Makova K.D., Adkins R.R., Glbson S., Li W.H.; Edizodic evolution of growth hormone in privates and emergence of the specificity of human growth hormone receptor."; Mol. Biol. Evol. 18:945-95(2001).

1- FUNCTION: Plays an important role in growth control. Its Title role in stimulation and profit is sto Silmingue the like liver and other Lissues to secrete (GFL). It stimulates both the differentiation and proliferation of Typhiass. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saimiri bollvionsis kollvionsis (Bollvian squiriel monkey).
Bukaryota: Matazoa: Chordata; Cranlala, Vertebrata: Burelessioni;
Mammalia: Buthoria; Primatos: Platyrrhini: Cebilae: Cabhbaer Saimiri
NGBI_TaxID-39432.
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-1- SUBCELLULAR LOCATION: Serreted.
-1- SIMILARITY: SELONGS TO THE SCHATCTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: Length 217;
  Length 217:
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57.7%; Score 460; DB 1;
98.9%; Pred. No. 5.8e-38;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                 28 FEB-203 (Rel. 41, Created)
28 FFB-2063 (Rel. 41, Last sequence update)
FEB-2003 (Rei. 41, Last annotation update)
Somatotropin precursor (Growth hormone).
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                                                                                                                                                                                     54.8%; Score 437; DB 91.3%; Pred. No. 1e-35
Live 5; Mismatches
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BY SIMILARITY.
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PROSITE: PSG0266; SOMATOTROPIN_1; 1.
PROSITE: PSG0338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF339660; AAK62287.1; -.
InterPro; IPR021400; Somatotropin.
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Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revol A. Esquivel D., Santiago D., Barrera-Saldana H.;
"independent duplication of the growth hormone gene in three
"independent lineages.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
PUNCTION: Plays an important role in growth control. Its major role in stimulating hody growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulate differentiation and proliferation of myoblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth hormone variant precursor (GH-V) (Placenta-specific growth hormone) (Growth hormone 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i-SUBCELLULAR LOCATION: Secreted.
-i-TISSUE SPECIFICITY: Expressed in the placenta.
-i-SIMILARITY: RELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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BY SIMILARITY.
BY SIMILARITY.
1592A429075677DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.5%; Score 434.5; DB 1; 78.9%; Pred. No. 1.8e-35; Weenstring 9;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                     AA.
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28-FEB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone, Placenta, Signal, Glycoprotein.
SignAL 1 26 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AF374233; AAL72265.1; -.
InterPro; IPRC01405; Somatotropin.
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215
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Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
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79
208
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P58757;
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                       SOM2_PANTE
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                                                                                                                                                                                                   RESULT 5
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Biol. Chem. 263:9001-9005(1988)
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MEDLINE-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99321812; PubMed-10393484;
    MEDLINE-83182010; PubMed=7169009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Senomics 4:479-497(1989).
                                                                                        DNA 1:239-249(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
                          Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumann G.
                                                                                                                                                                                                                                         proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVIEW.
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL cutstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-ssb.cf/announce/or send an email to licensellsb-sib.ch).
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                                                                                                                                                                                                                                                                                       -i- FUNCTION: Plays an important role in growth control. Its main role in stimulating body growth is to stimulate the liver and other tissues to secrete idP-1. It stimulates both the differentiation and proliferation of myobiasis. It also stimulates amino acid uptake and proliferation of myobiasis. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FPTIPLSRIEDNAMIRAHRIBGIAFOTYOEFREAYIPKEGKYSFLQNPOTSISFSESIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 FPTIPLSRILDMAMIRAHGHAFOTYQEFBBATIRROKYSFIONPQTSDFSFBPT
                                                                                                                                                                                                        Wails 0.0. Walls M.) "Cloning and characterisation of a putative growth hormone enceding gene from the marmose; (Callithrix jacobus)": Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
                                                                               Eukaryota, Metažos, Chordata, Cranidta, Vertebrara, Eutelwastemi).
Mammalia, Eutheria, Primates, Platyribick, Callifrichidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rol. 41, hast sequence update)
15-SSP-2003 (Rel. 42, Last endotation update)
Growth hormone variant precursor (GH-V) (Planenta-Specific growth
hormone) (Growth hormone 2).
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 217:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stopus
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BY SIMILARITY.
E162:51A12CE6192 CRC64:
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Pred. No. 3.26-35;
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PSNREETOOKSNLELLRISLLLIOSWLEPVQ 92
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                      Somatotropin predursor (Growth hormone) (GH).
                                                             Callithrix jacchus (Common marmoset).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00266; SOMATOTROPIN_1: 1. PROSITE; PS03389; SOMATOTROPIN_2: 1. Hormone; Pitultary; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR001400: Somatoiropin.
Pfam: PF00103: hormone; i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ297563; CAC03481.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24959 MW;
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91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
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                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID-9483;
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                                                                                                                             ithrix.
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A Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A HOPKINS R.P., Jordan B., Moore T., Mars S.L., Wang J., Hsieh F.,
A Eletchen M.J. Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J. Jsdh T.B., Toshlyuki S., Carninci P., Prange C.,
A Brownstein M.J. Jsdh T.B., Toshlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Jsdh T.B., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Morley K.C., Elete S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Kichards S., Worley K.C., Elete S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Kichards S., Worley K.C., Elete S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Kichards S., Worley K.C., Elete S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Kithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hirkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Bethery J., Helton D.K., Mrzywinski M.T., Skalska U., Smalus D.E.,
Bethery J., Marker M. S.C., Grimwood J., Schantuz J., Myers R.M.,
Betherfield Y.S.N., Krzywinski M.T., Skalska U., Smalus D.E.,
Chenertlon and intital analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Growth hormone heterogeneity in human pituitary and plasma.";
Horm. Res. 5 Suppl. 12-6(1999).
-!-PUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete 16F-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates action acid uptake and protoin synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'issues.
SUBUNIT: Monomer, dimer, trimer, tetramer and pentamer, disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linked or non-covalently associated, in homopolymeric and beteropolymeric combinations. Can also form a complex either with Subcellular Locations are secreted. Subcellular Locations Secreted.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The human growth hormone locus: nucleotide sequence, biology, and
                                                                                                                                                                                                                                                      REDITNE-E8243769; pubMed-3379057; Cooke N.E., RAY J., Emery C.G., Jebhabor S.A.; "Two distinct species of human growth formone-variant mRNA in the human placenta predict the expression of novel growth hormone.
"The Numan growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDGINE-89024584: PibMed-2460050.
MEDGINE-89024584: PibMed-2460050.
"Clouds and nucleotide sequence of placental hGH-V cDNA.";
Arch. Int. Physiol. Biochim. 96:63-67(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE~89307277; PubMed-2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A.,
Gelinas R.E., Sceburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. J.S.A. 99:16899-16903(2002).
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Name-1; Synonyms-GH-V1;
IsoId-P01242-1; Sequence-Displayed;
Name-2; Synonyms-GH-V2;
                                                                                                                                                                                                      SEĞUENCE FROM N.A. (ISOFORMS 1 AND 2).
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us-09-423-100-7.rsp

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Cercopithecinae, Macaca.
                                         NCBI_TaxID-9544;
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            $\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
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                                                                                                                                                    This SWISS-PROT entry is copyright, it is produced through a collaboration between the SWISS fistilate of Bioinformatics and the EMHL outstation the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Sue http://www.isb-sib.ch/announce/or send an email to licensetisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPTIPLSKLFDNAMLRAHFLHQLAFDTYQEFEEAYIPKHQKYSFLQNPQTSLSFSESIPT 61
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BY SIXIARITY.
N-LINKED (GICANG. . .) (FOIBNITAL.).
RLEDGRENGGIRNOSYSKEDIKSHNODALLKNYGLINGER
KOMDKVETELRIVQGRSVEGSGGF -> VRVARGIPHRGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LASRDWGEKHCCPLFSSQALTGENSPYSSFPLWNFPGLSTG
PGGGGKWMNERGREGGFSAWFLLLFUHFAEAGHWQTFFBAA
DLQSVLQQV (1b.18sform 2).
FILL-VSP_00623.
R >> W (1N.4bsNP-53489).
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Q07370; Q26494;
Q01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Growth hormone variant precursor (GH-V) (Placetta-specific growth)
hormone) (Growth hormone 2).
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Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteleosicmi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clycoprotein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      $3.5%: Score 426.5: DB 1: Length 217; Corsity 78.1%: Pred: No. 1.10.34: Conservative 4; Mismatches 10: Table 11.
                                                               -i- TISSUE SPECIFICITY: Explessed in the placenta.
-i- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROMATH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 -> T (IN REF. X).
7893246988822896 (RC64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROWTH HORMONE VARIANT
IsoId=P01242-2: Sequence=VSP_006203;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:4262; GH2.
MIN: 139240.
MO: GO:600518C; P:poptide hcrmone; TAS.
InterPro; FPR003406; Somatosropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00103; hormone: 1.
PROSITE: PS00266; SOMATCTROFIN_1;
PROSITE: PS00318: SOMATCTROFIN_2;
Hormone: Placenta: Signal: (lycopr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMB5, BCC20760, AAH20760.1; -. PIR: A28072; STHUV2. PIR: D32435; STHUV. HSSP: P01241; 1A22. Genew: HGNC:4262; GH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AA; 24999 MK;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K00470; AAA98619.1; --
EMBL; J03756; AAB59547.1; --
EMBL; J03756; AAR359549.1; --
EMBL; M34651; AAA35897.1; --
EMBL; J03071; AAA52552.1; --
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217
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SIGNAL
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Best Local Simi
Matches 89; (
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DISULFID
CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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ID DT DT OC OC OC OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 PSNKEETQOKSNLELLHISLLLIQSWLEPVQF-----LRSVFANHLVHTNSNFDIYLY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                          Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Cloning of four growth hormone/chorionic somatomammotropin-related complementary decoyribonucleic acids differentially expressed during pregancy in the rhesus monkey placenta.";
Endocrinology 133:1744-1752(1993).

"FUNCTION: Plays an important role in growth control. Its major role in stimulates the liver and other tissues to secrete 16F-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FPTIPLSRLFDNAMLRAHRIHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLUIAR LOCATION: Secreted (By similarity).
-:- TISSUE SPECIFICITY: Expressed in the placenta.
-:- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 217;
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                                                                    Sclos T.G.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
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EMBL; L15555; AAA2018G.i; -.
EMBL; 167411; 16741.
HSSP; P01241; 1HGG.
EnterPro; IPR001460; Somatotropin.
                                                                                                                                                                                                                                                                                             IISSUE=Placenta;
MEDLINE=94008724; PubMed-8404617;
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P01243;
21-JUL-1986 (Rel. 01, Created)
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SECUENCE FROM N.A.
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ANDURENT FROM TWA.

TISSUE-Placenta, and Uterus:

A Straubberg R.L., Pelnoold E.A., Orouse L.H., Berge J.G.,

REDLINE-22388257 PubMed=2477932

A Straubberg R.L., Collins F.A., Wagner I., Schaefer C.F., Beat R.K.,

A Altschul S.F., Zeeberg B., Bictow K.H., Schaefer C.F., Beat R.K.,

A Altschul S.F., Zeeberg B., Bictow K.H., Schaefer C.F., Beat R.K.,

A Altschul S.F., Zeeberg B., Bictow K.H., Schaefer C.F., Beat R.K.,

A Diatchenko L., Matusina K., Asamer A.A., Rubina G. M. Seneria F.L.,

Biotopheron M., Soares M.B., Bonaldo M.F., Casavar T.L., Schertz I.P.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavar T.L., Schertz I.P.,

Raba S.S., Loguellane N.A., Perers G.J., Abrasson B.C., Mulley S.B.,

Robards S.M., McEwar P.C., Mater S., Garcia A.M., Garsara R.C., Millon D.R., Matush D.M., Sodertan B.J., Hu X., Gibbs B.A.,

RA Nillalon D.R., Matay D.M., Sodertan B.J., Hu X., Gibbs B.A.,

Rabakelley R.W., Pourhman J.W., Green E.D., Dickenn W.C.,

RA Blakesley R.W., Tourhman J.W., Green E.D., Dickenn W.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smytlus D.S.,

Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smytlus D.S.,

RY Generation and initial acalysis of more than 15,000 full-length human and mouse cDNA sequences.",

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Lactogen precursor (Chorlomanmotropin) (Chorlonic secalemannotropin).
CSH1 AND CSH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (GENES CSH1 AND CSH2).
MEDLINE-89307277; Pubmed-2744760:
Cher E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The human growth hormone locus: nucleotide sequence, biclogy, and evolution.":
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                                                                                                             Eukaryota: Metazoa: Chordata: Craniata: Vertetrita: Eureleostom;;
Mammalia: Eutheria: Primates: Catarrhini; Bominidae: Home.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The human growth hormone gone family: buckeofide sequences show recont divergence and predict a new polypoptide hormone."; DNA 1:239-246(1982).
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MEDLINE-78071761; PubMed-593368;
Shine J., Seeburg P.H., Mart.al J.A., Baxter J.D., Goodman H.M.;
                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A. (GENE CSF2).
MEDLINE-87161235: PubMed-3050680;
Hirt H., Kimelman J., Birnbeum M.J., Chen R.Y., Scoburg P.H.,
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alielic variations.";
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MEDLINE~85030426: PUEMed*6208192;
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                                                                                                 Homo saplens (Human)
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SEQUENCE FROM N.A.
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P -> A (IN CSH2).
//TIId-VAR_007166.
IS -> L (IN CSH2).
//TIId-VAR_007167.
I -> T (IN REF. 9).
MISSING (IN REF. 9). "Construction and analysis of recombinant DNA for human chorionic semanementopin."; SECTENCE OF 27-217.
MEDLINE-73201971: PubMcd-4712450;
54 C.H., Bixon J.S., Chung D., Chung D., Amino acid Sequence of Incan chorionic sometomammotropin.":
Amino acid Sequence of Incan chorionic sometomammotropin.":
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PIR) C32435; LCHUC.
HSSP; P01241: IA22.
Genew: HGMC:2440; CSHI.
Genew: HGMC:2441; CSHI. Nature 270:494-499(1977). 217 215 215 208 225 3 84 95 116 507 SEQUENCE OF 27-117 27 79 208 208 215 84 95 116 104 SISULFID DISULFID DISULFID DISULFID InterPro: CONFLICT CONFLICT CONFLICT ERRATUM /ARIANT VARIANT CHAIN

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                                                                                                                                                                                                                        4 TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPCTSLSFSESTFTES 63
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Mammalia: Etheria: Rodenfia, Sciurognathi: Muridue, Cricellare,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-92063850; PubMed-1954881;
Southard J.N., Sanchez-Jimenez F., Campbell G.F., Talamantes F.;
"Sequence and expression of bamster prolactin and growth hermone
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                                                                                                   Length 217;
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BY SIMILARITY.
BY SIMILARITY.
3B69CE32AB6F1166 CRC54;
      SDD -> BBS (IN REF. 9).
- 235B0DC7A713F431 CRC64:
                                                               47.8%; Score 381; DS 1; for 82.0%; Pred. No. 3.20-30; Wiematches 8;
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01-0CT-1994 (Rel. 30, Last soquence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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PROSITE: PS00266; SOMATUTROP.N.;; 1.
PROSITE: PS0038; SOMATUTROP.N.2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salaenoptera borcalis (Sei whale).
Bukaryota: Metazoa: Chordata: Craniata; Vertebrata; Futeleostomi;
Marmalia: Futheria; Cotartiodactyla; Cetacca; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBCELULAR LCCATION: Secreted.
-:- SUBCELULAR LCCATION: Secreted.
-:- SIMICARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
PIR: PNG.40: PNG.40:
RSSF: PGL241; JAXI.
InterPro: JPRC04460; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
09FBFF6DB14A75D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yudaev N.A., Pankov V.A., Bulatov A.A., Osipova T.A.; "Amino acid sequence of sciwhale somatotropin.";
Blokbimiia 47:1059-1069(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
128-FEB-2003 (Rel. 41, Last annotation update)
Sommatotropin (Growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-3CE-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                      86 PIGKEEAQQRSOMELLRFSLLIZGSWLGPVQ 116
                                                                                                                                      92
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                                                                                                                                      62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ
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PROSITE, PS00266; SOMATOTROFIN_1; 1.
PROSITE; PS00338; SOMATOTROFIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDLINE-83000569; PubMed:7115813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balaenopteridae: Balaenoptera.
NCBI_TaxiD-9768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 AA; 21835 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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P01245;
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SOMA_HORSE
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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to sectete IOF: It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in miscie and other
                                                                                                                                                                                                                                                          [3]
MEDLINATY SEQUENCE OF 27-216.
MEDLINE-7402362: PubMed-4747845;
Zakin M.M., Poskus E., Dellacha J.M., Paladini A.C., Santose J.A.,
The amino acid sequence of equine growth hormone.";
PFHS Lett. 34:353-355(1973).
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 68-95 AND 183-216.
Zakin M.M., Poskus E., Dellacha J.M., Paladini A.C., Santume J.A.;
"Amino acid sequences around the cystine residues in equine drowth
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oliver L., Hartree A.S.;
"Amino acid sequences around the cystine residues in horse growth
                       Eguus caballus (Herse).
Bukaryota, Metazoa: Chordati, Craniata: Vertebrata: Buteleosicmi;
Mammalla: Butherla: Perissofactyla; Equidae: Equis.
                                                                                                                                                                                          MEDLINE-77005410: PubMed-965151;
Zakin M.M., Poskus E., Langton A.A., Ferrara i., Santome C.A.,
Dellacka J.M., Paladini A.C.;
Dellacka J.M., Paladini A.C.;
Interpretation of equips growth hormone.";
Int. J. Popt. Procein Res. 3:435-444 (1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.5%; Score 306.5; DB 1; Longth 216; 65.2%; Pred. No. 6.2e-23;
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SIMIDARITY: HELGNGS TO THE SCHAFOIRCPIN/FROLAGIIN PARTIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24423 MW; 37AB3173834011AC CRC64;
                                                                                                    TISSUE=Pitultary;
MEDJINE=94266171; PubMed-8236392;
Ascacio-Martinez J.A., Barrara-Saidaca H.A.;
Ascacio-Martinez D.A., Barrara-Saidaca H.A.;
Gene 143:299-330(1994);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMATOTROPIN
Somatotropin predursor (Growth Normone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03163; hormone; 1.
PROSITE; PS00266; SOMAIOTROFIN_1; 1.
PROSITE; PS06338; SOMATOTROFIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPROC1400; Somatofropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 202-216.
MEDLINE-68368390: PubMed-4676100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U02929; AAA21627.1; -.
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SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                normone.";
FEBS Lett. 25:77-82(1972).
                                                                                                                                                                                 SEQUENCE OF 27-216.
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                                                                                         SEQUENCE FROM N.A.
                                                               NCBI_TaxID=9796;
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20.6
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DISULFID
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Gaps

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Indels

14; Mismatches

Best Local Similarity 65.2% Matches 60: Conservative

Cuery Match

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1 :1: 1 1 :11 | :11 | :11: | :1: | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :1 | :
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"Bushbaby growth hormone is much more similar to comprimate growth
"Gromones than to thesus monkey and human growth hormones.";
Koi. Biol. Evol. 18:55-61(2001).
--- FUNCTION: Plays an important role in growth control. Its major
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Eukaryota, Metazoa: Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; GalagonIdae; Galago.
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ZFB61CD31136F0C5 CRC64:
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28-FES-2003 (Rel. 41, Last sequence update)
28-FES-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone).
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PROSTE; PSO0266; SCHATCHROPIN_1; 1.
PROSTE; PSO0338; SCHATCTROPIN_2; 1.
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InterPro: 1PR091406; Somatotropin.
Pfam, PF02163; hormone; 1.
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*! SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACIBN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (ACS-2000) to the EMBL/GenBack/HDBJ ditabases.
-!- FUNCTION: Plays an important role in growth control. Its majer role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulate amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                     Nycticebus pygmaeus (Pygmy słow loris).
Eukaryota, Metazoa, Chordata, Craniata: Vertebrata: Euteleostemi;
Mammalia: Eutheria; Primates: Strepsirhini; Loridae: Nycilcebus.
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65.2%; Pred. No. 6.2e<sup>-23</sup>;
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01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Srowth hormone).
                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone).
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Pfam: PF00103: bermone: 1.
PR1NTS; PR00836: SOMATUROPIN.
PR0SITE; PS00266: SOMATUROPIN.1: 1.
PR0SITE: PS00338: SOMATUROPIN.2: 1.
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between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/cr send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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-: FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and officer tissues to secrete 16F-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates anno acid uptake and protein synthesis in muscle and other
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                                                                                                                                                  SEQUENCE FROM N.A.
MEDIJNE-82561358; PubMed=2991252;
Linzar J.I.H., Talamantes F.;
Linzar D.I.H., Talamantes F.;
"Nuc.cotide sequence of muse prolactin and growth hormone mRNAs and expression of these mRNAs during pregnancy.";
J. Biol. Chem. 260:9574-9579(1985).
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRA.N-F27DU; TISSUB-Liver;
MEDIINF-96194803; PubMed-867448;
Das P. Meyer L., Seyfert H.-M., Brockmann G., Schwerin M.;
"Structure of the growth hormone-encoding gene and its promoter in
Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata: Cramiata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae: Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUNCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
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64.8%; Pred. No. 9.7e-23;
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAR. PSO0.03; hormone: 1.
PROSITE; PSO0.266; SOMATOTROPIN_1: 1.
PROSITE; PSO0.388; SOMATOTROPIN_2: 1.
BOTAGOO: Pituitary: Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X02891; CAA26650.1; -.
EMBL; 24663; CAA8658.1; -.
PIX; B2391; SEMS;
HSSP; P01246; 1BSr;
HSSP; P01246; 1BSr;
HGU; MG1:95707; Gh.
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78 189 BY
266 214 BY
216 AA; 24716 MW;
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                                                                                                NCBL_TaxID=10090;
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Gendore version 5.1.6
Copyright (c) 1993 - 2004 Compared 19.1.
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OM protein - protein search, using sw model

00 : Search time 36.1868 Seconds (Without Alignments) 1069.670 Million cell updates/sec September 16, 2003, 12:34:00 Run on:

US-09-423-100-7

981 NOAMETOATSOISTOCOM 129 1 MFPTIPESRIFONAMERAHR. Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapert 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 1938
Maximum Match 1938
Listing first 45 summaries

Database

sp_unclassif.ed:*
sp_rvirus:*
sp_bacteriap * sp_fungi:*
sp_human:*
sp_invertebra.e:*
sp_mammal:* sp_vertebrate:* sp_mhc:* sp_organello:* sp_phage:* sp_archea:*
sp_bacteria:* sp_rodent:* sp_virus:* sp_plant:* SPIREMBL 23:* Pred. No. is the number of results predicted by chance to have a score greater than or egual to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

SUMMARIES

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	436	54.7	217	ç	CBWNED	CSWD#O attractor
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m	407.5	51.1	217	9	007369	037 469 macana mana
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12	301.5	37.8	2.6	ç	OBEYES	OSEAS ATTRECOR
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16	297	37.3	217	9	08MI75	O8mi75 callithrix

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ALIGNMENTS

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62 PSNREETQCKSNLELLRISLLIQSWLEPVQLGTGPRFVNQHLCG-***--SHLVE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Platyrrhini: Cebidae; Atelinae; Ateles.
NCHI_TaxID~9509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A SEQUENCE FROM N.A.
A REVOLANCE FROM N.A.
A REVOLANCE SEQUENCE D., Santiago D., Barrera-Saldana H.;
A REVOLANCE SEQUENCE D., Santiago D., Barrera-Saldana H.;
Tradependent dupication of the growth hormone gene in three statements of the lineages."

Substituction (APR-2001) to the EMBL/GenBank/DDBC databases.

SEMBLY RATA224 AAL72286.1;

REMBLY PROSIDED AND SOM STORED OF THE SEQUENCE SEQUENCE SOM SOM STORED OF SEQUENCE SOM SOM STORED OF SEQUENCE STORED OF SEQUENCE 217 AA: 24884 MM: 425829FF41EFAARS CRC54;
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01-MAR-2002 (TrEMBLrel. 26, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                      Ateles geoffroyi (Black-handed spider monkey).
                                                                                      217 AA
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                                                                                      PRT;
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Hest Local Similarity 66.99
Matches 97, Conservative
                                                                                      PRELIMINARY;
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RESULT 1
                                             O8WNE0
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212 AA.
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                                               TiterPro; IPR001400; Somatotropin.
Pfam: PF00103; hormone: 1.
PR052TE; P800266; SOMATOTROPIN_1; 1.
PR05TIE; P500338; SOMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24874 MW: FIEB66
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Endocrinology 133:1744-1752(1993).
EMBL, L16554; AAA18841.1; -.
HSSP, P01241; 1AXI.
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                                                                                                                                                                                      Best Local Similarity 71.9%
Matches 82: Conservative
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MEDLINE-94008724; PubMed-8404617;
Golos T.G., Durning M., Fisher J.M., Fowler F.D.;
"Cloning of four growth hormone/chorisuic somatomasmetropin-related complementary deoxyribonucleic acids differentially expressed diring pregnancy in the rhesus monkey placental;";
                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of two novel growth hormone transcripts expressed in human placenta.":
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Mammalia, Eutheria: Primates: Catarrhini, Cercopitiecidae,
                                                                                                                                                                                                                                                             Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleosiemi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.6%; Score 427.5; D5 4: Longtis 245: Best Local Similarity 71.9%; Prod. No. 1.7e-37; Matches 92; Conservative 6; Mismatches 17: Indels 12
                                                                                                                                                                                                                                                                                                                                                   TISSUB-Term placenta;
MEDLINE=983737; Pubmed-9703963;
HOGUSZEW-KI C.L., Svensson P.A., Jansson T., Clark K.,
Carisson J.M.S., Carlsson B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIĞNAS 1 26 POTENTIAL.
SEQUENCE 245 AA: 27101 MW: 14CC7F8CD75091C8 CRC64;
                                                                                                                                                                    01-JAN-1996 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Placental growth hormone isoform hGH-V3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TEPMBLEEL 01, Created)
01-NOV-1996 (TEPMBLEEL 01, Last sequence update)
01-NAR-2003 (TEPMBLEEL 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Clin. Endocrinol. Metab. 83:2878-2865(1998).
EMBL: AF006051; AAB71829.1; ...
#SSP: P61241; IA22.
InterPro. IPR01450; Somatot.opin.
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                                                                                                                 245 AA
               146 GIGTLMGRIEDG---SPOTGEIFRG 167
                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Sreated)
01-JAN-1996 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last ann
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PROSITE, PS00266; SCMATUTROPIN_1; 1.
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
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                                                                                                                                014644;
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                                                                                                                                                                                    3 PTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEBAYIPKEQKYSFLQNPQTSLSFSESIPTP 62
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                                                                                                                                                                                                                     MEDLINE-94008724; PubMed-8404617; Golos T.G., Durning M., Fisher J.M., Fowler P.D.; Golos T.G., Durning M., Fisher J.M., Fowler P.D.; Colos T.G., Durning M., Fisher J.M., Fowler P.D.; Complementary Geoxytibonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta."; Endocrino.cgv 133:1744-1722(1993).

Endocrino.cgv 133:1744-1722(1993).

SISSE, PG.244, FAAI.

InterPro. 1PR0014001; Somatctropin.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                               63 SNREETQQKSNLSLLRISLLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEALYLV 116
                                                                                                                                                                                                                                                                                                                                             Bukaryota, Motazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Kammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                            DB 6; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrol. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAV-2003 (TrEMBLrel. 23, Last annotation update)
Somatotropin. 2 precursor (Growth hormone 2) (Fragment).
Macada mulatta (Rhesus macaque).
217 AA; 24874 MW; FIEBGAFDBBA:B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 AA; 24525 MW; 27BC91106256E6F5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 49.7%; Score 396; DB 6; L
Sest Local Similarity 92.2%; Pred. No. 2.6e-34;
Matches 74; Conservative 11; Mismatches 5;
                                                            51.1%; Score 407.5; DB 6; 71.9%; Pred. No. 1.6e-35; tive 12; Mismatches 19;
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us-09-423-100-7.rspt

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  J03071; AAA5253.1; -. BC022044; AAH22044.1; -. BC035965; AAH35965.1; -. P01241; 1A22.
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Best Local Similarity
Matches 69: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth hormone.
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Best Local Simil
Matches 73; (
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    EMBL;
EMBL;
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                                EMBL;
                                                 HSS5;
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01-NOV-1996 (TrEMBLrel, C1, Last Sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
Chortonic somatomammotropin CS-2 (Chorionic somatomammotropin hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89307277: PubMed-2744765;
Chen B.Y., Liao Y.C., Smith D.H., Barrera-Saldana B.A., Gelinss N.E.,
                                                                                              TISSUE-Midgregnancy placenta.

MEDLINE-94008724: PubMed-9404617;
GOLOS T.G., Durning M., Pisher D.M., Powier P.D.;
GOLOS T.G., Durning M., Pisher D.M., Powier P.D.;
Cloning of four growth cormone/choritonic somatememorropin-related complementary deoxyribonic.etc acids differentially expressed cortopinegrancy in the rhesus monkey placenta.";
Pregnancy in the rhesus monkey placenta.";
Pregnancy in the rhesus monkey placenta.";
PRMEL IL65522 AAALE839.1. ...
HSSP: PC1241: [AXI.
                                                                                                                                                                                                                                                                                                                                                   34158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vnencak-Jones C.L., Phillips J.A. 111., "Hot spots for growth hormone gene deletions in homologous regions outside of Alu repeats.";
              Eukaryota: Metazoa: Chordata: Craniata: Vertebruta: Euteleoatomi:
Mammalia: Eutheria: Primales: Catarrhini: Cerropitheeidae:
Cercopitheeinae: Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Motazoa, Chordata, Cramiata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhimi, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDbJ Jatabases.
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                                                                                                                                                                                                                                                         PRINTS; PROGRAG SONATOTROPIN, PROSITE; PSO0338: SOMATOTROFIN_2; 1. SEQUENCE 217 As: 24942 MW PPSAA9915131F2BG CRC64:
                                                                                                                                                                                                                                                                                                                  Ouery Match 49.7%; Secro 396; DB 6; Best Local Similarity 62.2%; Pred, No. 2.70-34; Matches 74; Conservative L:: Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 SNLEETQOKSNLELCRISLLALQSWLEPVQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  63 SNREETQQKSNLELLRISLLLLQSWLEPVQ 92
                                                                                                                                                                                                                                IPRC01400; Schatot.opin.
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Macada mulatta (Rhesus madagre)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 250:1745-1748(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 4:479-497(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                             Pfam: PFC0103; hormone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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SEQUENCE FROM N.A.
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                                                                                   SEQUENCE FROM N.A.
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                                                        NCBI_TaxID-9544;
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                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSRLFDNAMLRAHRLHOLAFDTYQEFEEAYIPKEOKYSFLCNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
                                                                                                                                                                                                                                                         Gaps
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Revol A., Esquivel D., Santiago D., Barrera-Saldana H.; "Independent duplication of the growth hormone gene in three
                                                                                                                                                                                                Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anthropoidean lineages.";
Submitted (APR-2001) to the EMBL/GenBauk/DDBJ databases
EMBL; AF374235, AAL72287.1;
LiterPro; IPRO1400; Somatotropin.
Ptan: PF00103; hormone: 1.
PRINTS: PR00836; SOMATOTROPIN.];
PROSTIE; PS00266 SOMATOTROPIN.];
PROSTIE; PS00266 SOMATOTROPIN.];
SROUGHUE: 217 AA; 25293 MW; 741745Alb75C053E CRC64;
                                                     PRINIS; PRO0836; SCMATOTROPIN.
PROSZTE; PS00236; SCMATOTROPIN.1: 1.
FROSZTE; PS00238; SCMATOTROPIN.2: 1.
SROUENCE 217 AA: 24994 MW: 39FAACDDB6B2E951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               014643 PRELIMINARY; PRT; 202 AA.
014643:
01-JAN-1598 (TYPMBLICEL. 05, Created)
01-JAN-1598 (TYPMBLICEL. 05, Last sequence update)
01-JUN-2062 (TYPMBLICEL. 21, Last annotation update)
Placental growth hormone 20kDa isoform precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CI "MAR-2002 (TrEMBLrel. 20, Created)
C1-MAR-2002 (TrEMBLrel. 26, Last sequence update)
C1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                             : Similarity 82.0%; Pred, No. 1.16-32; 3; Conservative 8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.7%; Score 348; DB 6; 75.6%; Pred. No. 3.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ateles geoffroyi (Black-handed spider monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              64 NREETOOKSNIELLRISLLLIQSWLEPVQ 92
EnterPro, IPR001460; Somatetropin.
Pfam; PF00103; hormone; 1.
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TISSUE=Liver;
                                                                                                                                                                                                                                   Nannospalax
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070615;
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                                                                                 RESULT 10
070615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PTIPLSRIFDNAMERAHRLHQLAPDIYQEFEEAYIPKEQKYSFLQNPQISLSFSESIPTP 62
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotu: Metazoa: Chordata Craniatu: Vertebrath, Eutoloestonu:
Mammalia: Euljeria: Primates Flatyrrbini: Callitrichidae: Callithix
                                                                                                                                                                                                                                                                                                                                                     26: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps ::
                                                                              TISSUE-Term placenta:
MEDLINE-9817373; PubMed-9789963;
Boguszewski C.L., Svensson P.A., Jansson T., Clark K.,
Carlsson J.M.S., Carlsson B.;
"Cloning of two novel growth hormone transcripts expressed in numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterisation of the GH gene cluster in a new-world monkey, town marmoset (calibhria Jacchus.";
Ju. Mol. Eddocrinol. 916-0(2002).
EMBL: AJ489811; CAD34512.1;
InterPro: PRF031400; Somatotropin.
Pfam: PF00103; hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                62 PSNREETQOKSNLELLAISLLLIQSWLEPVQL------GTGPRFVNQHL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                               72 PSNRVKTOOKSNJELLIGSTILLIGSWLEPVOLLKSVFANSLYYGASDSNVYRHH 125
               Craniala: Vertebraia: Euteleostori:
Catarrhici: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.5%; Score 322.5; DB 6; Length 217; Best Local Similarity 64.7%; Pred. No. 2e-26; Matches 66; Conservative 13; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                         42.6%; Shore 341; UB 4; Length 202; 65.6%; Pred. No. 1.9e-28;
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                                                                                                                                                                                                                                                                                                                                                     9: Indels
                                                                                                                                                                                                                                                                                              38B64D011A919706 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECF148798278F1A CRC64;
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01-0GT-2002 (TrEMBirel, 22, Last sequence indate)
01-MAR-2003 (TrEMBirel, 23, Last senotation update)
                                                                                                                                                            J. Clin. Endocrinol. Metab. 83:2878-2895(1999)
EMBL; AF006660; AAB71828.1; ..
HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT: 217 AA
                                                                                                                                                                                                                                                                                                                                                     4: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth hormone-like protein & precursor. GHLP6.
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                                                                                                                                                                                                                                                                                   POTENTIAL.
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PIGNET PRODUCTOR SOMATORIORIO.

PRINTS: PROCESS: SOMATORPORT.

PROSITE: PS00256: SOMATORPORT.

PROSITE: PS00338: SOMATORPORT.]:

1 PROSITE: PS00338: SOMATORPORT.]:
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SEQUENCE 202 AA; 23128 NW
              Eukaryota, Metazoa, Chordata
Mammalia, Eutheria, Primates
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27 217
217 AA; 25177 MW.
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.89
Matches 75, Conservative
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Wallis O.C., Wallis M.;
sapiens (Human).
                                                                  SEQUENCE FROM N.A
                                          NCBI_Tax12-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBL_TaxID 9483;
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Q8MI74
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Cetartiodactyla; Cetacea: Odontoceti: Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
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EMBL; AJ492191; CAD37292.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99124645; PubMed*9924177;
Lioupis A., Nevo E., Wallis M.;
"Cloning and characterisation of the gene encoding mole rat (Spalax
                                                                                                                                                                                                                                                                                                                                                                                        Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // Match 38.5%; Score 306.5; DB 11; Length 216; Local Similarity 65.9%; Pred. No. 1c-24; nes 65; Conservative 13; Mismatches 17; Indels 1;
                            88 FHKZEMLGKSNVELLHISTLLIQSWLEPKQ-RLGSIFANSQL 128
63 SNRRETOOKSNLELLRISLLLTOSWLEPVOLGTGPRFVNOHL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH HORMONE. : EEAB8A523BACADFF CRC64;
                                                                                                                                                                                                                                                                  C1-AUG-1998 (TrEMBLrel. 07, Created)
C1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
C1-AAR-2003 (TrEMBLrel. 23, Last annotation update)
Growth hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-00T-2002 (TrEMBLrel, 22, Created)
01-00T-2002 (TrEMBLrel, 22, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 PSNREETQQKSNLELLRISLLIQSWLEPVQ 92
                                                                                                                                                                                                               216 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001460; Somatotropin.
Pfam; PF63163; hormone; i.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.: 1.
PROSITE; PS00338; SOMATOTROPIN...; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Mol. Endocrinol. 22:29-36(1999).
EMBL: AJOS819; CAA06716.:; -.
HSSP; PO1241; JAXI.
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 216 G
216 AA; 24627 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ehrenbergi) growth hormone.";
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                                                                                                                                                                                                           PRELIMINARY;
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216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=30637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9728;
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PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                Best Local Similarity 63.7%
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB:_TaxID=9940;
                                                                                                                                                                                    Query Match
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ID 091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FPTIPLSRLFDNAMLRAHKLHQLAFDTYQEFERAYIFKEGKYSFLONPCISLSFSHSTPT 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i. Gaps
                                                                                                                                                            Science
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBL_TaxID-16090;
                                                                                                                                                                                                                                                                                                                                                                                                     Ailuropoda melanoleuca (Giant panda).
Wkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleustomi:
Mammalia, Eutheria, Carnivora, Fissipedia, Ursidae, Ailuropoda.
NCBI_TaxIb-9645,
                                                                                                                                                          -
                                                                                                                                58 6: Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.8%; Score 301.5; 58.6; Length 216;
64.8%; Pred. No. 3.46-24;
tive 14; Mismatches 17; Indols 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-FRIGHTARY:
TISSUE-FRIGHTARY:
"Closing and expression of cDNA encoding growth hormone from Aliuropoda melanoleca".
Abiluropoda melanoleca".
EMBL: AF540936: AN77228-11: -..
                                                                                          27 216 GROWTH HORMONE.
216 AA: 24509 NW: 1E0467A84CCFEB62 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL 1 26 POTENTIAL.
SEQUENCE 216 AA, 24383 MW; 44EC1?EC44RCR656 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Growth hormone precure andal.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                  37.8%; Score 301.5; DB 6;
64.8%; Prod. No. 3.48-24;
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86 PTGKDEAQORSDVELLRFSLLLIGSWLGPVU :16
                                                                                                                       Query Match
Best Local Similarity 64.84; Prod. No. New Best Local Similarity 64.84; Prod. No. New Matches 59; Conservative 14: Nismatches
                                                                                                                                                                                                                                   62 PSNREETQCKSNLELLRISLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                              216 AA
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                                                                               POTENTIAL
InterPro; ZPR01400; Scmatolropin.
Pfam; PF00103; hermone: 1.
PRINTS; PR00346; SOMATOTROPIN.
PROSTTE: PS00266; SOMATOTROPIN.
PROSTTE: PS00348; SOMATOTROPIN.
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Best Local Similarity 64.8%
Matches 59; Conservative
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                                                                                                       SEQUENCE
                                                                  Signal.
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                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                RESULT 12
QBHYE5
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Q9R2C3
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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lacroix M.C., Devinoy E., Servely J.L., Puissant C., Kann G.;
"Expression of the growth hormone gene in ovine placenta: detection and cellular localization of the protein.";
Endocrinology 137.4886-4892(1996).
BEBLS: C49063: AAC48679.1;
BSSP: P01241; 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pocora; Bovoidea;
Bovidae; Caprinae; Ovis
SEQUENCE FROM N.A. Not the brown state of the sequence and Phylogenetic "Mcuse Growth Hormone Locus: Nucleatide Sequence and Phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
r1
                                                                                                                                                                                                                                                                                                                                                                                                            37.5%; Score 298.5; DB 11; Length 216; 63.7%; Pred. No. 7.2e-24; ative 14; Mismatches 18; Indols 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.3%; Score 297.5; DB 6; Length 264; Rest Local Shmilarity 64.8%; Pred. No. 8.6e-24; Matches 59; Conservative 14; Mismatches 17; Indels 1.
                                                                            Analyses.";
Submitted (AUG-1985) to the EMBL/SenBank/SDBJ databases.
EMBL 054362; AAC99988.1; -.
R EMBL 054424; JAXI.
R Interpro; IPR001406; Somatotropin.
R PRINTS; PR00886. SOMATOTROPIN.
PRINTS; PR00886. SOMATOTROPIN.
PROSITE: PSCC266; SOMATOTROPIN.
PROSITE: PSCC266; SOMATOTROPIN.
SP PROSITE: PSCC386; SOMATOTROPIN.
SECUENCE 216 AA; 24682 NW; FC2A366DAC2536B18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 204 AA; 23462 MW; EBBB9451892635C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PSNREETOQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (IrEMBLrel, 52, Created)
01-FEB-1997 (TrEMBLrel, 52, Last seq:
01-MAR-2003 (TrEMBLrel, 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS00266, SOMATOTROPIN_1; 1. PROSITE, PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001400; Somatotropin.
Piam: PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta; MEDLINE=97050633; PubMed=8895361;
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01-0C7-2000 (TrEMBLrol. 15, (reated)
01-0C7-2000 (TrEMBLrol. 15, Last sequence update)
01-MAR-2003 (TrEMBLrol. 13, Last annotation update)
01-MAR-2003 (TrEMBLrol. 23, Last annotation update)
Growth hormone precursor.
Cavia porcellus (Guinea pig).
Cavia porcellus (Guinea pig).
Mammalia: Euthoria: Rodentia: Hystricognathi: Cavildae: Cavia.
MCBI_Taxib=10141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.3%; Score 297.5; EB 11; Length 216; Best Local Similarity 63.7%; Pred. No. 9.2e-24; Matches 58; Conservative 14; Mismatches 18; Indels 1;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
Odorico D.M., Fuller P.C., Herington A.C.;
Ucloning and sequence of quirea pig growth hormone (GR).";
Submitted (FEB-2000) to the EWBL/Genhauk/DDBH databases.
EMBL: AR233853, AAP$6409.1;
HSSP; P01241; 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
GROWTH HORMONE.
: 45996BEll9806DD3 CRC64:
 216 AA
                                                                                                                                                                                                                                                                                                          InterPro: IPR001400; Somatotropin.
Pfam: PF00103; hormone; IPR004836; SOMATOTROPIN.
PROSITE: PS00266; SOMATOTROPIN.
PROSITE: PS00338; SCMATOTROPIN...; I
 PRT;

    SIĞNAL
    1
    26
    P.

    CHAIN
    27
    216
    3

    SRQUENCE
    216
    AA:
    24822
    MW;

PRELIMINARY;
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                   Q9JKM4:
Q9JXM4
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62 PSNREETOOKSNIBSLRISILLIOSWIRPVO 92 :::1 | 1:1:: | 1:1:: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: | 1:1: đ ò ç d.

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Search completed: September 16, 2003, 12:40:01 Job time : 37:1868 secs